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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:20:54 ; Search time 135 Seconds
(without alignments)
760.153 Million cell updates/sec

Title: US-09-825-212-1

Perfect score: 1662

Sequence: 1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	100.0	320	10	US-09-825-212-1
2	1593	95.8	312	9	US-09-825-637-14
3	1593	95.8	312	14	US-10-084-205-14
4	1593	95.8	312	16	US-10-712-713-14
5	1582	95.2	311	16	US-10-787-887-2
6	1561	93.9	311	14	US-10-032-201B-265
7	1452	87.4	310	16	US-10-787-887-10
8	1154	69.4	315	12	US-10-290-072-66
9	1154	69.4	315	14	US-10-141-531-66
10	1154	69.4	315	14	US-10-032-201B-198
11	1145.5	68.9	315	12	US-10-032-201B-235
12	1145	68.9	316	12	US-10-290-072-103
13	1145	68.9	316	12	US-10-290-072-139
14	1145	68.9	316	14	US-10-141-531-103
15	1145	68.9	316	14	US-10-141-531-139

16	1144	68.8	316	12	US-10-290-072-148	Sequence 148, App
17	1144	68.8	316	14	US-10-141-531-148	Sequence 148, App
18	1143	68.8	316	12	US-10-290-072-85	Sequence 85, App
19	1143	68.8	316	12	US-10-290-072-130	Sequence 130, App
20	1143	68.8	316	14	US-10-141-531-85	Sequence 85, App
21	1143	68.8	316	14	US-10-141-531-130	Sequence 130, App
22	1141	68.7	316	12	US-10-290-072-184	Sequence 184, App
23	1141	68.7	316	14	US-10-141-531-184	Sequence 184, App
24	1137	68.4	316	12	US-10-290-072-112	Sequence 112, App
25	1137	68.4	316	12	US-10-290-072-157	Sequence 157, App
26	1137	68.4	316	14	US-10-141-531-112	Sequence 112, App
27	1137	68.4	316	14	US-10-141-531-157	Sequence 157, App
28	1137	68.4	316	14	US-10-141-531-175	Sequence 175, App
29	1137	68.4	316	12	US-10-290-072-94	Sequence 94, App
30	1136	68.4	316	12	US-10-290-072-121	Sequence 121, App
31	1136	68.4	316	12	US-10-290-072-193	Sequence 193, App
32	1136	68.4	316	14	US-10-141-531-94	Sequence 94, App
33	1136	68.4	316	14	US-10-141-531-121	Sequence 121, App
34	1136	68.4	316	14	US-10-141-531-193	Sequence 193, App
35	1136	68.4	316	12	US-10-290-072-166	Sequence 166, App
36	1135	68.3	316	14	US-10-141-531-166	Sequence 166, App
37	1135	68.3	316	12	US-10-290-072-202	Sequence 202, App
38	1134	68.2	316	14	US-10-141-531-202	Sequence 202, App
39	1134	68.2	316	14	US-10-032-201B-212	Sequence 212, App
40	1054	63.4	319	14	US-10-032-201B-253	Sequence 253, App
41	872	52.5	308	14	US-10-032-201B-268	Sequence 268, App
42	849	51.1	303	14	US-10-032-201B-243	Sequence 243, App
43	753	45.3	314	14	US-10-032-201B-244	Sequence 244, App
44	728.5	43.8	325	14	US-10-032-201B-208	Sequence 208, App
45	726	43.7	315	14		

ALIGNMENTS

RESULT 1

US-09-825-212-1
; Sequence 1, Application US/09825212
; Publication No. US20030166843A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Timothy E
; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF STAPHYLOCOCCUS AUREUS THIOREDOXIN REDUCTASE
; FILE REFERENCE: 00032.US1
; CURRENT APPLICATION NUMBER: US/09/825,212
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-825-212-1

Query Match 100.0%; Score 1662; DB 10; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.5e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEVENPFGFEMIT 60	
Db	1	MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEVENPFGFEMIT 60	
Qy	61	GPDLSTKMFHAKKPGAVVQGDIKSVDEKGEYKVINFGNKELTAKAVIATGASYKKTG 120	
Db	61	GPDLSTKMFHAKKPGAVVQGDIKSVDEKGEYKVINFGNKELTAKAVIATGASYKKTG 120	
Qy	121	VPGEELGGRGVSYCAVCDGAFFKNNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180	
Db	121	VPGEELGGRGVSYCAVCDGAFFKNNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180	
Qy	181	RAQRILQDRAFNKDKIDFINSHHTYSINEKDGKGSVTLTSTKDGSEETHEADGVFIYIG 240	

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Db 181 RAQRILQDRAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYG 240
QY 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
Db 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
QY 301 AAAYIEHLNDQARSHHHH 320
Db 301 AAAYIEHLNDQARSHHHH 320

RESULT 2
US-09-925-637-14
; Sequence 14, Application US/09925637
; Patent No. US2002010338A1
; GENERAL INFORMATION:
; APPLICANT: Choi
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
; FILE REFERENCE: PB560
; CURRENT APPLICATION NUMBER: US/09/925,637
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/151,933
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 08/781,986
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-637-14

Query Match 95.8%; Score 1593; DB 9; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
Db 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
Db 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
QY 121 VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
Db 121 VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
QY 181 RAQRILQDRAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYG 240
Db 181 RAQRILQDRAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYG 240
QY 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
Db 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
QY 301 AAAYIEHLNDQAR 312
Db 301 AAAYIEHLNDQAR 312

RESULT 3
US-10-084-205-14
; Sequence 14, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/712,713
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-084-205-14

Query Match 95.8%; Score 1593; DB 16; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
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; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-084-205-14

Query Match 95.8%; Score 1593; DB 14; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
Db 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
Db 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
QY 121 VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
Db 121 VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
QY 181 RAQRILQDRAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYG 240
Db 181 RAQRILQDRAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYG 240
QY 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
Db 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
QY 301 AAAYIEHLNDQAR 312
Db 301 AAAYIEHLNDQAR 312

RESULT 4
US-10-712-713-14
; Sequence 14, Application US/10712713
; Publication No. US20040082002A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/712,713
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-712-713-14

Query Match 95.8%; Score 1593; DB 16; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
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Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGTEIDFIALIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMIT 60
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QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIG 120
Db 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIG 120
QY 121 VPGEQLGGRGVSVCVCDGAFKKNKLFVITGGGDSAVEEGTFTTKFADKVTIIVHREDEL 180
Db 121 VPGEQLGGRGVSVCVCDGAFKKNKLFVITGGGDSAVEEGTFTTKFADKVTIIVHREDEL 180
QY 181 RAQILQDRAFKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIG 240
Db 181 RAQILQDRAFKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIG 240
QY 241 MKPLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQS 300
Db 241 MKPLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQS 300
QY 301 AAEYIEHLNDQA 312
Db 301 AAEYIEHLNDQA 312

RESULT 5
US-10-787-887-2
; Sequence 2, Application US/10787887
; Publication No. US20040161809A1
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Borovok, Ilya
; APPLICANT: Cohen, Gerald
; APPLICANT: Uziel, Orit
; APPLICANT: Katz, Leonard
; TITLE OF INVENTION: Recombinant Staphylococcus aureus Thioredoxin Reductase
; FILE REFERENCE: 85189-899
; CURRENT APPLICATION NUMBER: US/10/787,887
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/076,525
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: US 09/261,301
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-787-887-2

Query Match 95.2%; Score 1582; DB 16; Length 311;
Best Local Similarity 99.4%; Pred. No. 1.8e-140;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TEIDFIALIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 62
Db 2 TEIDFIALIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVP 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVP 121
QY 123 GEQELGGRGVSVCVCDGAFKKNKLFVITGGGDSAVEEGTFTTKFADKVTIIVHREDELRA 182
Db 122 GEQELGGRGVSVCVCDGAFKKNKLFVITGGGDSAVEEGTFTTKFADKVTIIVHREDELRA 181
QY 183 QRILQDRAFKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 242
Db 182 QRILQDRAFKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 241

QY 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQSAA 302
Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQSAA 301
QY 303 EYIEHLNDQA 312
Db 302 EYIEHLNDQA 311

RESULT 7
US-10-787-887-10
; Sequence 10, Application US/10787887
; Publication No. US20040161809A1
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Borovok, Ilya
; APPLICANT: Cohen, Gerald
; APPLICANT: Uziel, Orit

QY 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQSAA 302
Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQSAA 301
QY 303 EYIEHLNDQA 312
Db 302 EYIEHLNDQA 311

RESULT 6
US-10-032-201B-265
; Sequence 265, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-032-201B-265

Query Match 93.9%; Score 1561; DB 14; Length 311;
Best Local Similarity 98.1%; Pred. No. 1.7e-138;
Matches 304; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 TEIDFIALIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 62
Db 2 TEIDFIALIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVP 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVP 121
QY 123 GEQELGGRGVSVCVCDGAFKKNKLFVITGGGDSAVEEGTFTTKFADKVTIIVHREDELRA 182
Db 122 GEQELGGRGVSVCVCDGAFKKNKLFVITGGGDSAVEEGTFTTKFADKVTIIVHREDELRA 181
QY 183 QRILQDRAFKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 242
Db 182 QRILQDRAFKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 241
QY 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQSAA 302
Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIPAGDVDRDKGLRQIVTATGDSIAAQSAA 301
QY 303 EYIEHLNDQA 312
Db 302 EYIEHLNDQA 311

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; APPLICANT: Katz, Leonard
; TITLE OF INVENTION: Recombinant Staphylococcus Thioredoxin Reductase
; FILE REFERENCE: 85189-899
; CURRENT APPLICATION NUMBER: US/10/787,887
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/076,525
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: US 09/261,301
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-787-887-10

Query Match      87.4%; Score 1452; DB 16; Length 310;
Best Local Similarity 89.9%; Pred. No. 3.2e-128;
Matches 277; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP 62
Db 2 TEVDFVAILIIGAGPAGMTAAVYASRANLKTVMIERGMFGQMANTEEVENFPGFEMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGV 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINLGNKEITAHAVIISTGAAYKKIGV 121
QY 123 GEQLGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRA 182
Db 122 GEQLGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRA 181
QY 183 QRILQDRAFNKDKIDFWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
Db 182 QNIIQERAFNKDKVDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQA 302
Db 242 PLTAPFKNLGITNDAGYIVTQDDMTSKVRGIFAAGDVRDKGLRQIVTATGDSIAAQA 301
QY 303 EYIEHLND 310
Db 302 DYITELKD 309

RESULT 8
US-10-290-072-66
; Sequence 66, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
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; LENGTH: 315
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-290-072-66

Query Match      69.4%; Score 1154; DB 12; Length 315;
Best Local Similarity 71.4%; Pred. No. 3.9e-100;
Matches 220; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITG 66
Db 6 YDVIITIGAGPAGMTAAVYTSRANLSTLMIERGIPGGQMANTEDVENYPGFESILG 65
QY 67 KMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGV 126
Db 66 KMFHAKKFGAVYQYGDIKSVEDKGYKVKVAGSKEVKARAVIIAAGAEYKKIGV 125
QY 127 LGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRA 186
Db 126 LGGRGVSVCADGAFKFKGKELVVVGSGDSABEGVYLTRFASKVTIVHRRDKLR 185
QY 187 QDRAFNKDKIDFWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 246
Db 186 QARAFDNEKVDLWNTVKIHEENGKVGNTLVDTVTGSESEKTDGVFIYIGMLPLSK 245
QY 247 PFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQA 306
Db 246 PFENLGITNEEGVIEINDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQA 305
QY 307 HLNDQARS 314
Db 306 ELQETLTK 313

RESULT 9
US-10-141-531-66
; Sequence 66, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-141-531-66

Query Match      69.4%; Score 1154; DB 14; Length 315;
Best Local Similarity 71.4%; Pred. No. 3.9e-100;
Matches 220; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITG 66
Db 6 YDVIITIGAGPAGMTAAVYTSRANLSTLMIERGIPGGQMANTEDVENYPGFESILG 65
QY 67 KMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGV 126
Db 66 KMFHAKKFGAVYQYGDIKSVEDKGYKVKVAGSKEVKARAVIIAAGAEYKKIGV 125
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; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacillus subtilis variant
US-10-290-072-103

Query Match      68.9%; Score 1145; DB 12; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

QY 1 MGTEDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENPPGEMIT 60
Db 1 MSEEKIYDVIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENYPPGESIL 60

QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKG 120
Db 61 GPESLNKMFHAKKFGAEYAYGDIKEVIDGKEYKVKVAGSKYKARAVIIAAGAEYKKG 120

QY 121 VPGEQLGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
Db 121 VPGEKELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGVYLTFRASKVTIVHRYDKL 180

QY 181 RAQRILQDRAFKNDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSETHEDAGVFIYIG 240
Db 181 NAQSILQARAFDNEKVDLWNTKVEIHEENGKGVNVLVDVTGGESEFKTDGVFIYIG 240

QY 241 MKPLTAPFKDLGINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQS 300
Db 241 MLPLSKPENIGITNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300

QY 301 AAETIEHLNDQARS 314
Db 301 VQHVVEELQETLTKT 314

RESULT 13
US-10-290-072-139
; Sequence 139, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 316
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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacillus subtilis variant
US-10-290-072-139

Query Match      68.9%; Score 1145; DB 12; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

QY 1 MGTEDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENPPGEMIT 60
Db 1 MSEEKIYDVIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENYPPGESIL 60

QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKG 120
Db 61 GPESLNKMFHAKKFGAEYAYGDIKEVIDGKEYKVKVAGSKYKARAVIIAAGAEYKKG 120

QY 121 VPGEQLGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
Db 121 VPGEKELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGVYLTFRASKVTIVHRYDKL 180

QY 181 RAQRILQDRAFKNDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSETHEDAGVFIYIG 240
Db 181 NAQSILQARAFDNEKVDLWNTKVEIHEENGKGVNVLVDVTGGESEFKTDGVFIYIG 240

QY 241 MKPLTAPFKDLGINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQS 300
Db 241 MLPLSKPENIGITNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300

QY 301 AAETIEHLNDQARS 314
Db 301 VQHVVEELQETLTKT 314

RESULT 14
US-10-141-531-103
; Sequence 103, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacillus subtilis variant
US-10-141-531-103

Query Match      68.9%; Score 1145; DB 14; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

QY 1 MGTEDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENPPGEMIT 60
Db 1 MSEEKIYDVIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENYPPGESIL 60
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Db      241  MLPSPKPNIGITNEEGYIETNDRMETKVEGIFAGDIREKSLRQIVTATGDSIAAOS 300
QY      301  AAETIEHLNDOARS 314
      ||| : :
Db      301  VOHYVEELQETLKT 314

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Job time : 136 secs

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Search completed: September 15, 2004, 12:32:46
Job time : 136 secs

[illegible]

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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:16:13 ; Search time 32 Seconds
(without alignments)
516.260 Million cell updates/sec

Title: US-09-825-212-1

Perfect score: 1662

Sequence: 1 MGTEIDFDIAIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/2/iaa/5A COMB.pap.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pap.*
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4: /cgn2_6/prodata/2/iaa/6B COMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1083	65.2	253	4	US-09-134-001C-5512
2	940	56.6	310	4	US-09-134-000C-5514
3	618	37.2	317	4	US-09-328-352-8114
4	607	36.5	320	4	US-09-328-352-5678
5	594	35.7	311	4	US-09-198-452A-331
6	581	35.0	339	4	US-09-543-681A-5633
7	579.5	34.9	333	4	US-09-598-747-25
8	575	34.6	300	4	US-09-598-747-7
9	571.5	34.4	329	4	US-09-134-000C-3897
10	565.5	34.3	321	4	US-09-540-014-25
11	568.5	34.2	349	4	US-09-489-039A-12096
12	559	33.6	332	4	US-09-540-014-24
13	549.5	33.1	323	4	US-09-252-991A-29849
14	524.5	31.6	332	4	US-09-540-014-9
15	513.5	30.9	334	1	US-08-386-729A-7
16	497.5	29.9	310	4	US-09-598-747-27
17	484.5	29.2	301	4	US-09-598-747-6
18	482	29.0	510	1	US-08-220-677A-2
19	455	27.4	522	4	US-09-252-991A-28463
20	454	27.3	523	4	US-09-328-352-6394
21	454	27.3	523	4	US-09-328-352-6395
22	449.5	27.0	524	4	US-09-540-236-2706
23	443	26.7	508	4	US-09-134-001C-4570
24	436	26.2	512	4	US-09-107-532A-6559
25	415	25.0	538	4	US-09-543-681A-4490
26	369.5	22.2	87	4	US-09-134-001C-5497
27	300.5	18.1	339	4	US-09-107-532A-6420

28 285.5 17.2 199 4 US-09-252-991A-31441 Sequence 31441, A
29 279 16.8 215 4 US-09-252-991A-31700 Sequence 31700, A
30 273 16.4 192 4 US-09-489-039A-13402 Sequence 13402, A
31 253 15.2 553 4 US-09-134-001C-2974 Sequence 2974, Ap
32 238 14.3 334 4 US-09-134-000C-5068 Sequence 5068, Ap
33 234 14.1 507 4 US-09-091-097-34 Sequence 34, Appl
34 233 14.0 507 4 US-09-091-097-10 Sequence 10, Appl
35 225 13.5 474 4 US-09-556-877-90 Sequence 90, Appl
36 225 13.5 474 4 US-09-620-412C-90 Sequence 90, Appl
37 225 13.5 474 4 US-09-410-568-90 Sequence 90, Appl
38 225 13.5 474 4 US-09-598-419-90 Sequence 90, Appl
39 218.5 13.1 496 4 US-09-328-352-6168 Sequence 6168, Ap
40 215 12.9 456 4 US-09-252-991A-28041 Sequence 28041, A
41 212 12.8 491 4 US-09-262-856A-5 Sequence 5, Appl
42 210 12.6 473 4 US-09-134-001C-3405 Sequence 3405, Ap
43 210 12.6 479 4 US-09-252-991A-25982 Sequence 25982, A
44 204 12.3 480 4 US-09-252-991A-32853 Sequence 32853, A
45 199 12.0 484 4 US-09-543-681A-5905 Sequence 5905, Ap

ALIGNMENTS

RESULT 1

US-09-134-001C-5512
; Sequence 5512, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5512
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5512

Query Match 65.2%; Score 1083; DB 4; Length 253;
Best Local Similarity 85.7%; Pred. No. 5,5e-100;
Matches 209; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 67 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGQE 126
Db 9 KCLNMLKNLVAEYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGQE 68
QY 127 LGGRGVSYCAVDCGAFKKNKELFVIGGDSAVEGTFKTKFADKVTIVHRRDELRAQIL 186
Db 69 LGGRGVSYCAVDCGAFKKNKELFVIGGDSAVEGTFKTKFADKVTIVHRRDELRAQIL 128
QY 187 QDRAPKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTDKGSETHADGVFIYIGMKPLTA 246
Db 129 QERAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTDKGSETHADGVFIYIGMKPLTA 188
QY 247 PFKDLGTNDVGYIVTKDDMTSTVPGIFAGDVRDKGLRQIVTATGDSIAQAASAEYIE 306
Db 189 PFKNLGTNDVGYIVTKDDMTSTVPGIFAGDVRDKGLRQIVTATGDSIAQAASAEYIE 248
QY 307 HLND 310
Db 249 ELKD 252

RESULT 2

US-09-134-000C-5514
; Sequence 5514, Application US/09134000C

Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5514
LENGTH: 310
TYPE: PR
ORGANISM: Enterococcus faecalis
US-09-134-000C-5514

Query Match 56.8%; Score 940; DB 4; Length 310;
Best Local Similarity 58.9%; Pred. No. 1.4e-85;
Matches 178; Conservative 42; Mismatches 82; Indels 0; Gaps 0;

QY 7 FDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTVEENPPGPEMITGPDLSK 66
DB 8 YDVIILGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTVEENPPGPEMITGPDLSK 67

QY 67 KMEHAKKFGAVYQYGDIKSVDEKGYKVINFGNKGKLTAKAVIATGAEYKKGIVPGQEL 126
DB 68 KMYENVEKGTENAGYIWMGIEDHGSYKVEICDDKSYEAKAVIATGAEYKKGIVPGQEL 127

QY 127 LGRGVSVCACDGAFFKPKRLFVIGGDSAVEGFTTTFKADKVTIVHRRDELRAQRI 186
DB 128 FAGRGVSVCACDGAFFKPKRLFVIGGDSAVEGFTTTFKADKVTIVHRRDELRAQRI 187

QY 187 QDRAFNKDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
DB 188 QDRAFANEKISFVWDTVVEIIVGNEMVTVGVKARNVKTDEVSEIEANGVFIYIGMKPLTA 247

QY 247 PFKDLGINTDVGIVTKDDMTTSVPGIFAGDVDRDKGLRQIVATGDSIAAQ 299
DB 248 PFKAGITNAGMTIETQEMRTKIPVYAGDVDRDKGLRQIVATGDSIAAQ 299

QY 307 HL 308
DB 308 EL 309

RESULT 3
US-09-328-352-8114
Sequence 8114, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8114
LENGTH: 317
TYPE: PR
ORGANISM: Acinetobacter baumannii
US-09-328-352-8114

Query Match 37.2%; Score 618; DB 4; Length 317;
Best Local Similarity 44.1%; Pred. No. 1.9e-53;
Matches 137; Conservative 53; Mismatches 111; Indels 10; Gaps 4;

QY 9 IAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTVEENPPGPEMITGPDLSK 67
DB 8 LIILGSGPAGYSAVYAAARANKPTLIAGLQGLQGLTTTTEVDNPNPGLTGPALMDR 67

QY 68 MFEHAKKFGAVYQYGDIKSVDEKGYKVINFGNKGKLTAKAVIATGAEYKKGIVPGQEL 127
DB 68 MQAHERFGTELVDYHINEVDLNVFPFVLKGMEEVTCDAIIATGATAQYLGLESEQNF 127

QY 128 GGRGVSVCACDGAFFKPKRLFVIGGDSAVEGFTTTFKADKVTIVHRRDELRAQRI 187
DB 128 MQQGVSAACATCDGFFYKQKVMVVGNGNTAVEEALYLSNIAHVTIVHRRDLSRSEKILQ 187

QY 188 DRAF---KNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPL 244
DB 188 DHLFVKEKEGKISIVWNHEVEVLGNTGTVTSLRKLSTODESKQDVEVHGLFVAIGYKPN 247

QY 245 TAPFKDLGINTDVGIVTKDDMT-----TSVPGIFAGDVDRDKGLRQIVATGDSIAAQ 299
DB 248 TGMF-DGQLNLRDGYIQVSGTSGNATATSVAGVFAAGDVADSIYRQAITSGAGGMAAL 306

QY 300 SAAEYIEHLND 310
DB 307 DAEKYLQDND 317

RESULT 4
US-09-328-352-5678
Sequence 5678, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5678
LENGTH: 320
TYPE: PR
ORGANISM: Acinetobacter baumannii
US-09-328-352-5678

Query Match 36.5%; Score 607; DB 4; Length 320;
Best Local Similarity 43.4%; Pred. No. 2.4e-52;
Matches 134; Conservative 55; Mismatches 110; Indels 10; Gaps 4;

QY 9 IAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTVEENPPGPEMITGPDLSK 67
DB 13 LIILGSGPAGYSAVYAAARANKPTLIAGLQGLQGLTTTTEVDNPNPGLTGPALMDR 72

QY 68 MFEHAKKFGAVYQYGDIKSVDEKGYKVINFGNKGKLTAKAVIATGAEYKKGIVPGQEL 127
DB 73 MQAHERFGTELVDYHINEVDLNVFPFVLKGMDEYTCDAIIATGATAQYLGLESEQNF 132

QY 128 GGRGVSVCACDGAFFKPKRLFVIGGDSAVEGFTTTFKADKVTIVHRRDELRAQRI 187
DB 133 MQQGVSAACATCDGFFYKQKVMVVGNGNTAVEEALYLSNIAHVTIVHRRDLSRSEKILQ 192

QY 188 DRAF---KNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPL 244
DB 193 DHLFAKEKEGKISIVWNHEVEVLGNTGTVTGVLKSTKDKSKQEVQVQGLFIAIGHKPN 252

QY 245 TAPFKDLGINTDVGIVTKDDMT-----TSVPGIFAGDVDRDKGLRQIVATGDSIAAQ 299
DB 253 TSMFEGQLNLRD-GYIQVSGTSGNATATSVAGVFAAGDVADSIYRQAITSGAGGMAAL 311

QY 300 SAAEYIEHL 308
DB 312 DAEKYLQDND 320

RESULT 5
US-09-198-452A-331
Sequence 331, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:

9 IAIIGAPGAGTAAYVASRANLKTVMIERICPGQOMANTEEVENPFG-EMITGPDLSLK 67
 :
 29 LIILGSPGAGTAAYVAARANLEPVLTGVKXGQLTTTTEVWNPFGDEGUTGGLMDR 88
 :
 68 MEEHAKFQAVYGYGIKSVEDGE-YKVINFQN-KELTAKAVIATGAAYKKIVGPGEQ 125
 :

Patent No. 6531648

Patent No. 6531648

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; GENERAL INFORMATION:
; APPLICANT: Lanahan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus
US-09-598-747-7

Query Match      34.6%; Score 575; DB 4; Length 300;
Best Local Similarity 43.2%; Pred. No. 3.4e-49; Indels 6; Gaps 6;
Matches 130; Conservative 53; Mismatches 112;

QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGFEMITGPDLSL 66
DB 2 YDVAIIGGAGLTAALYSARYGLKTVFFETVDPVSLSLAAKIENYVPGPEG-SGMELLE 60
QY 67 KMFEHAKKFGAVYQYGDIKSVDEKGE-YKVINFGNKELTAKAVIIATGAAYKKIGVPEQ 125
DB 61 KMKEQAVKAGAEKWKLEKVERVNERGETFTVIAEGG-EYEAKAIIVATGGKHKEAGITEG 119
QY 126 ELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGFTTKFKADKVTIVHRRDELRAQRI 185
DB 120 AFITGRGVSYCATCDGNFFRGKVVIVGSGKEAIEDAILYHDIGCEVTIVSRTSFRACKA 179
QY 186 LQRAFKNDKIDFTWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYGMKPLT 245
DB 180 LVVEVEKRG-IPVHYSTIRKI-IGSGKVEKVAYNREKKEFEIEADGIFVAIGMRPAT 237
QY 246 APFKDLGITND-VGYIVTKDDMTSVPGIFPAAGDVROKGLRQIVTATGDSIAQAASAEY 304
DB 238 DWAEELGVDSMGYIKVDKEQRTNVEGVFAAGDCDNLKQVVVTACDGDGAAVAYSAYKY 297
QY 305 I 305
DB 298 L 298

RESULT 9
US-09-134-000C-3897
; Sequence 3897, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3897
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3897

Query Match      34.4%; Score 571.5; DB 4; Length 329;
Best Local Similarity 39.0%; Pred. No. 8.6e-49; Indels 7; Gaps 3;
Matches 120; Conservative 58; Mismatches 123;

QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGFEMITGP 62

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DB 22 TEEIYDLIIIGGSAALSAGIYAGRAMDMLIIKDKIGQGVTTTSEIUNYVPAIRHTTGP 81
QY 63 DLSTKMFESHAKKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIIATGAAYKKIGVP 122
DB 82 ELMBEEMRTQAOFGVAFNTDEIIDVFSQTIKTQSASQTYQAYAVLIATGASARKIGFP 141
QY 123 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGFTTKFKADKVTIVHRRDELRA 182
DB 142 GSEETGRGVAYCSTCDGFEFFQGLDFVIGGGVAAAEAAVLTFRYKSVTMIIREPDFTC 201
QY 183 QRILQDRAFNKIDKIDFWSHTTKSINEKDKGVSVTLTSTKDGSEETHEAD----GVFI 237
DB 202 AKLTAAEAAKNHPKIKIVYNIYEVKEIT-GDDFVRKAVFVNNQGTGETVYEPKDXSTGFLFV 260
QY 238 YIGMKPLTAPFKDLGITNDVGYIVTKDDMTSVPGIFPAAGDVROKGLRQIVTATGDSIA 297
DB 261 FAGNKPESTEIFEG-KIALDRGYVPTTENMETNIPGYAAGDLRIKELRQIVTAVADGAIA 319
QY 298 AQSAAEYI 305
DB 320 ATHAQRVY 327

RESULT 10
US-09-540-014-25
; Sequence 25, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-540-014-25

Query Match      34.3%; Score 569.5; DB 4; Length 321;
Best Local Similarity 42.1%; Pred. No. 1.3e-48;
Matches 136; Conservative 55; Mismatches 115; Indels 17; Gaps 8;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGF-EMI 59
DB 1 MGTTKHKSLLILGSGPAGYTAAYAAANLQFLVITGMEKGGQLTTTTEVENWFGDPNDL 60
QY 60 TGPDLSTKMFESHAKKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIIATGAAYKKI 119
DB 61 TGPLLMERMEHATKFEIIFDHLINKVDLQNRPFRLNGDNGEYTCDAIIATGASARYL 120
QY 120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGFTTKFKADKVTIVHRRDE 179
DB 121 GLPSEAPFKRGVSCATCDGFFYRNQKVAVIGGNTAVEEALYUSNTIASEVHLIHRDGG 180
QY 180 LRAQRILODRAFNKIDKID-FIWSHTTKSINEKDKG--VGSVTLTSTKDGSE-ETHEAD 233
DB 181 FRAEKILIKRLM--DKVNGNIIILHNTLEBVTGDMQVTVRLRDLRTQNSDNIESLDVA 238

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QY 234 GVFYIVGMKLPAPPK-DLGIITNDVGYIIVTKDDM-----TTSVPGIFAAGDVDRDKGLROI 287
Db 239 GLFVAIGHSPNTAIFEGOLELEN--GYIKVQSIIHCNATQTISIPGVFAAGDVMHDHYROA 296

QY 288 VTATGGSTAAQAARAEYIEHLND 310
Db 297 ITSAGTGCAALDAERYLDGLAD 319

RESULT 11
US-09-489-039A-12096
; Sequence 12096, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 2709.2084001
; CURRENT FILING DATE: US/09/489, 039A
; PRIOR APPLICATION NUMBER: 2000-01-27
; PRIOR FILING DATE: US 60/117,747
; NUMBER OF SEQ ID NOS: 1999-01-29
; SEQ ID NO 12096
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12096

Query Match 34.2%; Score 568.5; DB 4; Length 349;
Best Local Similarity 40.7%; Pred. No. 1.9e-48;
Matches 136; Conservative 51; Mismatches 114; Indels 33; Gaps 8;

QY 1 MGTEIDPDIAIIGAGPAGMTAAVVASRANLKTYMIERGIPCGQMANTVEENPPGP-EMI 59
Db 28 MGTAKSKLLILGSGPAGYTAANYAARANLOPVLIITGMERGGQLTTTTEVENWPGDENL 87

QY 60 TGPLSTKMPEHAKFGAVYYQGDIKSVE-----DKGEVKVINFGNKELTAKAVI 109
Db 88 TGPLLMEHHAAKETEIIHFHSRVDLQNRPFLRTGDSGY-----TCDALI 137

QY 110 IATGAEVKKIGVPEGDELGRGSYSYACDGAFKNKRLFVI GGGSASVEEGTFTTKFAD 169
Db 138 IATGASARYLGLPSEAFKRGVSACATCDGFFRYRNQKAVI GGNATAVEEALYLSNIAS 197

QY 170 KVTVIHRRDELAQRILQDRAFNKDIDFTWSHTTKSINEKCK---VGSVTILTSTKDG 226
Db 198 EVELHIHRSDSFRAEKLLIKELMDKVASGNVLVHTRILEVTGDQMGVGLRLDRDTKNSD 257

QY 227 E-ETHEADGVFIYGMPKTAPPK-DLGITNDVGYIIVTKDDM-----TTSVPGIPAAGDV 279
Db 258 NYVESLEVAGLFVAIGHSPNTAIFEGOLELEN--GYIKVQSIIHCNATQTISIPGVFAAGDV 315

QY 280 RDKGLRQIVTATGDSIIAQSAAEYIEHLNQAR 313
Db 316 MDHYRQAITSGTGCMAALDAERYLDGLADACK 349

RESULT 12
US-09-540-014-24
; Sequence 24, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540, 014

193 RASKIMQARALSNPKIQVWMD---SEVVVAYGAGGGLAGVKVKNLVTGEVSDLOVSGSL 249
236 FYIYGMKPLTAPFKDLGITNDVGYIVTVDKDMT-TSVPGIFAAAGDVDRKGLRQIVTATGDG 294
250 FPAIGHPEPATKFLNQLHLDADYVATKPGSTHTSVGVFAAGDVQDKKYRQAITAAGSG 309
295 SIAQSAABEYIEHLNDQ 311
310 CWAALDAEHLQEVGAQ 326

RESULT 15
US-08-386-729A-7
; Sequence 7, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yossef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattavilder, Alfred
; APPLICANT: Pallisa, Harriet
; TITLE OF INVENTION: An oxido reductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; TITLE OF INVENTION: production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weil, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-024/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-386-729A-7

17 VILIGSGPAGYGAAYFAARANKPLLIITGMQAGGLTITTEVDNPNPDPHGHTGALMOR 76
68 MEHAKKFCNAVQYQGDIVKVEDKGEYKVFNGKELTAKAVIATGAAYKKIIGVPGQEL 127
77 MQEHAERFETEIVFOHIAHVDLAGKFTLRGNGIYTCALIVATGASARYLGLPSEQAF 136
128 GGRGVSYCAVCDGAFKFKRLFYIGGDSAVREGTFTTKFADKVTIVHRRDELRAQRILO 187
137 MKGVSAACATCDGFFVYRNEVAVIGGNTAVEEALYLANIAGRVTLVHRRFTRAEKILQ 196
188 DRAFKNDKIDFINSHTTKSINEKDGKGVSVT--LTSTKGSBETHADGVFIYGMKPLT 245
197 DKLQARVAEGKIVLKLNAEYDEVLGDTMGVTGRLKTRDGSSEIADVGMFVAIGHPTNT 256
246 APPKDLGITNDVGYIVTK-----DDMTTSPVGFIAAGDVDRKGLRQIVTATGDGSAAGS 300
257 SLFEGQIALKD-GYLVVNGREGNATATNPGVFAAGDVADHVYRQAITAGAGCMAALD 315
301 AAEYIEHL 308
316 VERYLDSL 323

RESULT 14
US-09-540-014-9
; Sequence 9, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-540-014-9

Query Match
Best Local Similarity 31.6%; Score 524.5; DB 4; Length 332;
Matches 124; Conservative 44; Mismatches 132; Indels 17; Gaps 6;
9 IAIIGAGPAGTAAVYASRANKVTMIERGI-----PGSQMANTTEVENPFGFEM-ITGP 62
13 VCIIGSGPAAHTAAIYAAARALKPVLFEQGMANDIAAGQLTTTDDVENPFGPFGIMGI 72
63 DLSTKMFHAKKFGAVYQYQCDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIIGVP 122
73 DLMNCRAGSVRFGTILSETVEVDSARPPRVTSSTTVLADTVVATGAVARLHFS 132
123 GQELGGRGVSYCAVCDGA--FPFKRLFVIGGDSAVREGTFTTKFADKVTIVHRRDEL 180
133 GSDTYNNRGISACAVCDGAAPFRNKPFAVIGGDSAMBEQGNFLTKYGSQVYIIHRRNTP 192
181 RAQRILQDRAFKNDKIDFIWHSHTTKSINEKDGKGVSVTLTSTK-----DGSEETHRADGV 235

Search completed: September 15, 2004, 12:22:10
Job time : 33 secs

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result No.	Score	Query Match	Length	DB	ID	Description
1	1662	100.0	320	5	ABB04148	Abb04148 Recombina
2	1593	95.8	312	4	AAU00834	Aau00834 S. aureus
3	1592	95.2	311	6	ABM72250	Abm72250 Staphyloc
4	1573	94.6	309	6	ADA89500	Ada89500 Staphyloc
5	1561	93.9	311	2	AAV29854	Aav29854 Staphyloc
6	1561	93.9	311	5	ABP60916	Abp60916 Staphyloc
7	1455	87.5	310	2	AAV29855	Aav29855 Staphyloc
8	1455	87.5	310	4	AA62024	Aag2024 S. epider
9	1154	69.4	315	5	ABP60849	Abp60849 Bacillus
10	1154	69.4	315	6	AAO20618	Aao20618 Thioredox
11	1154	69.4	315	7	ADD26553	Add26553 B. subtil
12	1152	69.3	315	6	AAO20627	Aao20627 Thioredox
13	1145.5	68.9	315	5	ABP60886	Abp60886 Bacillus
14	1090	65.6	309	7	ADD26570	Add26570 B. subtil
15	1083	65.2	253	5	ABP40667	Abp40667 Staphyloc
16	1054	63.4	319	5	ABP60863	Abp60863 Listeria
17	1054	63.4	319	5	ABBA49968	Abb49968 Listeria
18	929.5	55.9	324	6	ADB088826	Abd08826 Alloioococ
19	899	54.1	305	5	ABP26879	Abp26879 Streptococ
20	872	52.5	308	5	ABBS4256	Abbs4256 Lactococcc
21	872	52.5	308	5	ABP60904	Abp60904 Lactococcc
22	852.5	51.3	304	5	ABP26878	Abp26878 Streptococ
23	849	51.1	303	5	ABP60919	Abp60919 Streptococ
24	849	51.1	303	6	ABU01907	Abu01907 S. pneumo
25	753	45.3	314	5	ABP60894	Abp60894 Clostridi

WO200177309-A2.
18-OCT-2001.
03-APR-2001; 2001WO-US010678.
06-APR-2000; 2000US-0195055P.
(PHAA) PHARMACIA & UPOJOHN CO.
Benson TE;
MPI; 2002-034237/04.
Crystallizing Staphylococcus aureus thioredoxin reductase molecule or molecular complex by preparing purified thioredoxin reductase and crystallizing from solution comprising dimethyl sulfoxide and sodium formate.
Claim 52; Fig 11; 147pp; English.
The present sequence is that of a recombinant Staphylococcus aureus thioredoxin reductase ("rx8") the crystal structure of which is solved in the specification. Thioredoxin reductase is a two domain protein composed of a flavin adenine dinucleotide (FAD) binding domain and a reduced beta-nicotinamide adenine dinucleotide phosphate (NADPH) binding domain. The specification describes the crystallisation of S. aureus thioredoxin reductase molecule or molecular complex. The crystal of the invention may be used to design an inhibitor of S. aureus thioredoxin reductase activity. The method is useful for crystallising a S. aureus thioredoxin reductase molecule or molecular complex. The crystal obtained is useful for solving the structure of other molecules or molecular complexes and designing inhibitors of S. aureus thioredoxin reductase. A composition comprising the inhibitor is useful for preventing and treating S. aureus thioredoxin reductase mediated disease

XX	Sequence 320 AA;
SQ	
	Query Match 100.0%; Score 1662; DB 5; Length 320;
	Best Local Similarity 100.0%; Pred. No. 3e-146; Indels 0; Gaps 0;
	Matches 320; Conservative 0; Mismatches 0;
QY	1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPPGFEMIT 60
Db	1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPPGFEMIT 60
QY	61 GPDLSTKMFEEHAKKFGAVQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
Db	61 GPDLSTKMFEEHAKKFGAVQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
QY	121 VPQEQLGGRGVSYCAVCDGAFFKNKELFVI GGSDSAVEEGTFPTKEADKVTIVHRRDEL 180
Db	121 VPQEQLGGRGVSYCAVCDGAFFKNKELFVI GGSDSAVEEGTFPTKEADKVTIVHRRDEL 180
QY	181 RAQRILLQDRAFKNDKIDFIWSHTTKSINEKDGVSGVTLTSKDGSEETHADGVFIYIG 240
Db	181 RAQRILLQDRAFKNDKIDFIWSHTTKSINEKDGVSGVTLTSKDGSEETHADGVFIYIG 240
QY	241 MKPLTAPFKDLGITNDVGYYIVTKDDMTTSVPGIFAAGDVDRDKGLRQIVTATGDGSIAAQS 300
Db	241 MKPLTAPFKDLGITNDVGYYIVTKDDMTTSVPGIFAAGDVDRDKGLRQIVTATGDGSIAAQS 300
QY	301 AAEYIEHLNQARSHHHHH 320
Db	301 AAEYIEHLNQARSHHHHH 320
RESULT 2	
AAU00834	
ID	AAU00834 standard; protein; 312 AA.
XX	
AC	AAU00834;
XX	
DT	04-JUL-2001 (first entry)
XX	
DE	S. aureus thioredoxin reductase, TrxB.
XX	
KW	Thioredoxin reductase; TrxB; immunogen; vaccine; antibody;
KW	wound infection; cellulitis; burn infection; eyelid infection;
KW	food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis;
KW	skin infection; scalded skin syndrome; toxic epidermal necrosis;
KW	Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis.
XX	
OS	Staphylococcus aureus.
XX	
FH	Key Location/Qualifiers
FT	Region 192..194
FT	/label= Antigenic_epitope
FT	Region 210..212
FT	/label= Antigenic_epitope
XX	
PN	WO200116292-A2.
XX	
PD	08-MAR-2001.
XX	
PF	31-AUG-2000; 2000WO-US023773.
XX	
PR	01-SEP-1999; 99US-0151933P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Choi GH;
XX	
DR	WPI; 2001-183259/18.
XX	
DR	N-PSDB; AAS00915.
XX	
Pt	New isolated nucleic acid for use in diagnosing Staphylococcus infections.
Pt	and in vaccines for eliciting immune responses to the infections.

Claim 9; Page 16; 235pp; English.

The sequence represents *S. aureus* TrxB (Thioredoxin reductase). The polynucleotides of the invention are used to detect *Staphylococcus* nucleic acids in a biological sample from an animal for diagnosing *Staphylococcus* infections. The polypeptides of the invention are used to detect anti-*Staphylococcus* antibodies in a biological sample from an animal to diagnose *Staphylococcus* infections. The polypeptides are also used in vaccines to elicit protective antibodies. The polypeptides are also of the *Staphylococcus* genus and for preventing or attenuating an infection caused by a member of the *Staphylococcus* genus e.g wound infection, cellulitis, burn infection, eyelid infection, food poisoning, joint infection, neonatal conjunctivitis, osteomyelitis, skin infection, scalded skin syndrome (also known as toxic epidermal necrosis, Ritter's disease and Lyell's disease), toxic shock syndrome and endocarditis. The polynucleotides may also be used in vaccines and for preventing or attenuating a *Staphylococcus* infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in *in vitro* and *in vivo* diagnostic and therapeutic methods

Sequence 312 AA:

Query Match	95.8%;	Score 1593;	DB 4;	Length 312;
Best Local Similarity	99.4%;	Pred. No. 7.7e-140;		
Matches 310;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			
QY	1	MGTEIDFDIAIIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPFGFEMIT	60	
Db	1	MGTEIDFDIAIIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPFGFEMIT	60	
QY	61	GPDLSTKMFCHAKFKGAVIYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG	120	
Db	61	GPDLSTKMFCHAKFKGAVIYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG	120	
QY	121	VPGEQLGGRGVSYCAVCDGAFPNKKRLFVIGGDSAVEEGTATTFADKVTIVHRRDEL	180	
Db	121	VPGEQLGGRGVSYCAVCDGAFPNKKRLFVIGGDSAVEEGTATTFADKVTIVHRRDEL	180	
QY	181	RAQRILQDRAFNKDKIDFTWSHTTKSINEKDGKVGSVTLTSTVGGSEETHADGVFIYIG	240	
Db	181	RAQRILQDRAFNKDKIDFTWSHTTKSINEKDGKVGSVTLTSTVGGSEETHADGVFIYIG	240	
QY	241	MKPLTAPFKDLGITNDVGIVYVTDMMTTSVPGIFAAGDVDRDKLROI VATDGSIAAQS	300	
Db	241	MKPLTAPFKDLGITNDVGIVYVTDMMTTSVPGIFAAGDVDRDKLROI VATDGSIAAQS	300	
QY	301	AAEYIEHLNDQA	312	
Db	301	AAEYIEHLNDQA	312	

RESULT 3	
ABM72250	
ID	ABM72250 standard; protein; 311 AA.
XX	
AC	ABM72250;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Staphylococcus aureus protein #1490.
XX	
KW	Antibacterial; vaccine; infection; sepsis; diagnosis;
KW	enzymatic assay; antibiotic target.
XX	
OS	Staphylococcus aureus.
XX	
PN	WC200294868-A2.
XX	
PD	28-NOV-2002.
XX	
PF	27-MAR-2002; 2002NO-IB0002637.
XX	

PR 27-MAR-2001; 2001GB-00007661.
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX
PI Masignani V, Mora M, Scarselli M;
XX
XX WFI; 2003-120786/11.
DR N-PSDB; ACF73810.
DR

PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
PT

PS Claim 1; SEQ ID NO 2980; 49pp; English.

The invention relates to novel genes and encoded proteins from *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to *Staphylococcus* bacteria, specifically an infection caused by *S. aureus*. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel *S. aureus* proteins of the invention.

SQ Sequence 311 AA;

Query Match 95.2%; Score 1582; DB 6; Length 311;
Best Local Similarity 99.4%; Pred. No. 8.1e-139;
Matches 308; Conservative 0; Mismatches 2; Indels

	QY	3	TEIDFDIAIIGAGPAGMTAAVYSRANLKTVMIERGIPGGQMANTEEVENPGFEMITGP	62
	Ddb	2	TEIDFDIAIIGAGPAGMTAAVYSRANLKTVMIERGIPGGQMANTEEVENPGFEMITGP	61
	QY	63	DLSTKMFHAHKGAVYYQGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP	122
	Ddb	62	DLSTKMFHAHKGAVYYQGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP	121
	QY	123	GEOELGGRGVSYCAVCDGAFNNKL FVI GGDSDSAVERGTFTTKPADKVTIVHRDELR A	182
	Ddb	122	GEOELGGRGVSYCAVCDGAFNNKL FVI GGDSDSAVERGTFTTKPADKVTIVHRDELR A	181
	QY	183	QRILQRAFNDKI DFIWSHTTKTSNEKDGVGSVTLTSTDGSGSEETHEADGVPI YIGMK	242
	bB	182	QR ILQRAFNDKI DFI WSH TL K TS NE KD GV GS V T L T S TD G SG SE E TH EA DG VP I Y IG MK	241
	QY	243	PLTAPFKD LG IT ND VG Y IV TKDDMTTS VPGI PA AGDV RD KL R Q IV T AT GDG SI AA QS AA	302
	bB	242	PLTAPFKD LG IT ND VG Y IV TKDDMTTS VPGI PA AGDV RD KL R Q IV T AT GDG SI AA QS AA	301
	QY	303	EYIEHLNDOA 312 	
	bB	302	EYIEHLNDOA 311 	

RESULT 4
ADA89500
ID ADA89500 standard; protein; 309 AA.

ADA89500;

T 20-NOV-2003 (first entry)

Staphylococcus aureus antigenic protein #39.

antigenic protein; vaccine; *Staphylococcus aureus*; pathogenic organism;
antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
antiulcer; immunostimulant; ophthalmological; pathogenic microbe;
bacteremia; septic shock; organ infection; skin infection;
bacterial basal colonisation; bacterial eye infection; septicæmia;
tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;

sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 gastro-enteritis; dysentery; shigellosis; skin disorder.
 Staphylococcus aureus.
 WO2003011899-A2.
 13-FEB-2003.
 02-AUG-2002; 2002WO-GB003606.
 02-AUG-2001; 2001GB-00018825.
 09-JAN-2002; 2002GB-00000349.
 (UYSH-) UNIV SHEFFIELD.
 (BIOS-) BIOSYNEXUS INC.
 Foster S, Mond J, Clarke S, McDowell P, Brummel K;
 WPI; 2003-256434/25.
 New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 useful as a vaccine for immunizing humans against e.g. bacteremia, septic
 shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
 impetigo.
 Claim 4; Page 131; 189pp; English.
 The present invention describes an antigenic protein or its part, which
 is for use as a vaccine. The antigenic protein is encoded by an isolated
 DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
 sequences (designated dnaa and dna SE, respectively); and which encodes a
 protein expressed by a pathogenic organism. Also described: (1) a vaccine
 composition comprising at least one antigenic protein; (2) a method of
 immunising an animal against a disease or condition caused by a
 pathogenic microbe by administering the antigenic protein or the vaccine;
 (3) an antibody or its binding part obtainable by the method above; (4)
 preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 hybridoma cell line produced by the method of (4); and (6) identifying
 opsonic antigens expressed by a pathogenic microbe. The antigenic
 proteins have antibacterial, neuroprotective, immunosuppressive,
 anti-inflammatory, antitumor, immunostimulant and ophthalmological
 activities, and can be used in vaccines. The antigenic proteins or
 vaccines can be used for immunising an animal (specifically a human)
 against a disease or condition caused by a pathogenic microbe, e.g.
 bacteraemia, septic shock, organ infection, skin infection, bacterial
 basal colonisation, bacterial eye infections, septicaemia, peritonitis,
 bacteria-associated food poisoning, blood infections, gonorrhoea,
 endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
 strep throat, streptococcal-associated toxic shock, necrotising
 fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 dysentery, shigellosis, S. aureus-associated septicaemia, food poisoning,
 skin disorders, S. epidermidis-associated septicaemia, peritonitis or
 endocarditis. The present sequence represents a S. aureus antigenic
 protein sequence from the present invention.
 Query Match 94.6%; Score 1573; DB 6; Length 309;
 Best Local Similarity 99.4%; Pred. No. 5.6e-138;
 Matches 306; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 3 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFGFEMITGP 62
 2 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFGFEMITGP 61
 63 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVINFGNKELTAKAVIATGAEYKKGIVP 122
 62 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVINFGNKELTAKAVIATGAEYKKGIVP 121
 123 GEQELGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182

Db 122 GEQELGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFKNDKIDFIWSHTTKSINEXDGVKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFKNDKIDFIWSHTTKSINEXDGVKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVRDKGLRQIVTATGDSIAAQAASAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVRDKGLRQIVTATGDSIAAQAASAA 301
 Qy 303 EYIEHLND 310
 Db 302 EYIEHLND 309
 RESULT 5
 AAY29854
 ID AAY29854 standard; protein; 311 AA.
 AC AAY29854;
 DT 17-NOV-1999 (first entry)
 XX Staphylococcus aureus trx8 open reading frame protein sequence.
 DE Staphylococcus; trx8; thioredoxin reductase; antimicrobial.
 KW Staphylococcus aureus.
 OS Staphylococcus aureus.
 XX WO9945123-A1.
 XX 10-SEP-1999.
 XX 02-MAR-1999; 99WO-US004512.
 XX 02-MAR-1998; 98US-0076525P.
 XX (ABBO) ABBOTT LAB.
 XX Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;
 PI WPI; 1999-551044/46.
 XX N-PSDB; AAZ21080.
 XX A new thioredoxin reductase from Staphylococcus aureus.
 PT Claim 2; Fig 2; 59pp; English.
 XX The present sequence represents Staphylococcus thioredoxin reductase
 (TrxB). TrxB inhibitors can be used as antimicrobials to treat a
 Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are
 antimicrobials to which, unlike most of those in the prior art,
 Staphylococcus has not yet developed a resistance
 SQ Sequence 311 AA;
 Query Match 93.9%; Score 1561; DB 2; Length 311;
 Best Local Similarity 98.1%; Pred. No. 7.4e-137;
 Matches 304; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 3 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFGFEMITGP 62
 2 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFGFEMITGP 61
 63 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVINFGNKELTAKAVIATGAEYKKGIVP 122
 62 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVINFGNKELTAKAVIATGAEYKKGIVP 121
 123 GEQELGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
 122 GEQELGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFKNDKIDFIWSHTTKSINEXDGVKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242

Db 182 QRILQDRAFKNDKIDFIWSHTLKSINEKDGKVGSVTLSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSA 302
 Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSTS 301
 Qy 303 EYIEHLNDQA 312
 Db 302 GYIEHLNDQA 311

RESULT 6

ABP60916
 ID ABP60916 standard; protein; 311 AA.

XX AC
 XX XX
 XX XX

DT 06-SEP-2002 (first entry)

XX Staphylococcus aureus thioredoxin reductase SEQ ID NO:265.
 XX

KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KW vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.

XX Staphylococcus aureus.
 OS

XX WO200250289-A1.
 PN

XX 27-JUN-2002.
 PD

XX 19-DEC-2001; 2001WO-US050240.
 PF

XX 19-DEC-2000; 2000US-00742900.
 PR

XX 05-JUL-2001; 2001US-0302885P.
 PR

XX 04-DEC-2001; 2001US-00006038.
 PR

PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA

XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX

PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX

DR WPI; 2002-508806/54.
 DR

XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.

XX Claim 82; Page 315-316; 362pp; English.
 PS

XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD); cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease (COPD); cataracts,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD

CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 311 AA;

Query Match 93.9%; Score 1561; DB 5; Length 311;
 Best Local Similarity 98.1%; Pred. No. 7.4e-137;
 Matches 304; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPPGFEMITGP 62
 Db 2 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPPGFEMITGP 61
 Qy 63 DLSTKMEFAHAKFGAVYQYGDIIKSVEDKGEYKVINFGNKELTAKAVIIATGAEEKYKIGVP 122
 Db 62 DLSTKMEFAHAKFGAVYQYGDIIKSVEDKGEYKVINFGNKELTAKAVIIATGAEEKYKIGVP 121
 Qy 123 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
 Db 122 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFKNDKIDFIWSHTLKSINEKDGKVGSVTLSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFKNDKIDFIWSHTLKSINEKDGKVGSVTLSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSA 302
 Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSTS 301
 Qy 303 EYIEHLNDQA 312
 Db 302 GYIEHLNDQA 311

RESULT 7

AAV29855
 ID AAV29855 standard; protein; 310 AA.

XX AC
 XX AAV29855;

XX DT 17-NOV-1999 (first entry)
 XX

DE Staphylococcus epidermidis trxB open reading frame protein sequence.
 XX

KW Staphylococcus; trxB; thioredoxin reductase; antimicrobial.
 XX

OS Staphylococcus epidermidis.
 XX

XX WO9945123-A1.
 PN

XX 10-SEP-1999.
 PD

XX 02-MAR-1999; 99WO-US004512.
 PF

XX 02-MAR-1998; 98US-0076525P.
 PR

XX (ABBO) ABBOTT LAB.
 PA

XX Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;
 PI

XX WPI; 1999-551044/46.
 DR

XX N-PSDB; AAZ221081.
 DR

XX A new thioredoxin reductase from Staphylococcus aureus.
 PT

XX Claim 2; Fig 7; 59pp; English.
 PS

XX The present sequence represents Staphylococcus thioredoxin reductase
 CC (TrxB). TrxB inhibitors can be used as antimicrobials to treat a
 CC Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are
 CC antimicrobials to which, unlike most of those in the prior art,
 CC Staphylococcus has not yet developed a resistance

XX Sequence 310 AA;
SQ Query Match 87.5%; Score 1455; DB 2; Length 310;
Best Local Similarity 90.3%; Pred. No. 5.6e-127;
Matches 278; Conservative 17; Mismatches 13; Indels 0; Gaps 0;
QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTTEVENPFGFEMITGP 62
Db 2 TEVDFDVAIIGAGPAGMTAAVYASRANLKTVMIERGMPGGQWANTTEVENPFGFEMITGP 61
QY 63 DLSTKMFHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKGIVP 122
Db 62 DLSTKMFHAKFGAEYQYGDIKSVEDKGDYKVINLGNKEITAHAVIISTGAEYKKGIVP 121
QY 123 GEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
Db 122 GEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 181
QY 183 QRILQDPAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHEADGVFIYIGMK 242
Db 182 QNIIQERAFKNDKVDFIWSHTLTKINEKDGKGVSVTLSTKDGAEQYDADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGVYIVTKDMMTTSVPGIFAAGDVDRDKGLRQIVTATGDSIAAQSAA 302
Db 242 PLTAPFKNLGITNDAGYIVTQDDMSTKVRGIFAAGDVDRDKGLRQIVTATGDSIAAQSAA 301
QY 303 EYIEHLND 310
Db 302 DYITELKD 309
RESULT 9
ID ABP60849 standard; protein; 315 AA.
XX AC ABP60849;
XX DT 07-AUG-2003 (revised)
XX DT 06-SEP-2002 (first entry)
XX DE Bacillus subtilis thioresoxin reductase SEQ ID NO:198.
XX KW Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
KW vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW gastro intestinal bleeding; malignancy; reperfusion injury; wound healing;
KW gastro oesophageal reflux disease.
XX OS Bacillus subtilis.
XX OS WO200250289-A1.
XX PD 27-JUN-2002.
XX PF 19-DEC-2001; 2001WO-US050240.

XX Sequence 310 AA;
SQ Query Match 87.5%; Score 1455; DB 2; Length 310;
Best Local Similarity 90.3%; Pred. No. 5.6e-127;
Matches 278; Conservative 17; Mismatches 13; Indels 0; Gaps 0;
QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTTEVENPFGFEMITGP 62
Db 2 TEVDFDVAIIGAGPAGMTAAVYASRANLKTVMIERGMPGGQWANTTEVENPFGFEMITGP 61
QY 63 DLSTKMFHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKGIVP 122
Db 62 DLSTKMFHAKFGAEYQYGDIKSVEDKGDYKVINLGNKEITAHAVIISTGAEYKKGIVP 121
QY 123 GEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
Db 122 GEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 181
QY 183 QRILQDPAFNKDKIDFIWSHTTKSINEKDGKGVSVTLSTKDGSEETHEADGVFIYIGMK 242
Db 182 QNIIQERAFKNDKVDFIWSHTLTKINEKDGKGVSVTLSTKDGAEQYDADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGVYIVTKDMMTTSVPGIFAAGDVDRDKGLRQIVTATGDSIAAQSAA 302
Db 242 PLTAPFKNLGITNDAGYIVTQDDMSTKVRGIFAAGDVDRDKGLRQIVTATGDSIAAQSAA 301
QY 303 EYIEHLND 310
Db 302 DYITELKD 309
RESULT 8
ID AAG82024 standard; protein; 310 AA.
XX AC AAG82024;
XX DT 03-SEP-2001 (first entry)
XX DE S. epidermidis open reading frame protein sequence SEQ ID NO:1142.
XX KW Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;
KW endocarditis.
XX OS Staphylococcus epidermidis.
XX PN WO200134809-A2.
XX PD 17-MAY-2001.
XX PF 09-NOV-2000; 2000WO-US030782.
XX PR 09-NOV-1999; 99US-0164258P.
XX PA (GLAXO) GLAXO GROUP LTD.
XX PI Kimmerly WJ;
XX DR WPI; 2001-316495/33.
XX DR N-PSDB; AAH52874.
XX KW Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
KW useful for vaccinating against infections, e.g. endocarditis.
XX PS Claim 18; Page 330; 2188pp; English.
XX CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (ii), given in AAG81454 to AAG8120, from Staphylococcus epidermidis. (I)
CC and (II) can have antibacterial activity and therefore can be used in
CC vaccination. The nucleic acids (II) may be used to produce the S.
CC epidermidis polypeptides (II) via the production of vectors containing
CC them which are used to produce hosts cells which express the

CC lung injury. This sequence represents a thioredoxin reductase variant
CC protein of the invention
XX
SQ Sequence 315 AA;
Query Match 69.4%; Score 1154; DB 6; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.5e-99;
Matches 220; Conservative 33; Mismatches 55; Indels 0; Gaps 0;
QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENPFGFEMITGPDLSL 66
DB 6 YDVIITIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENYPGFESILGPESLN 65
QY 67 KMFEHAKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKIGVPGEOE 126
DB 66 KMFEHAKFGAEYAGYDKEVIDGKEYKVKVAGSKYKARAVIIAAGAEYKKIGVPGEKE 125
QY 127 LGGRGVSYCAVCDGAFKKNKELFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
DB 126 LGGRGVSYCAVCDGAFKKGKELVVGSGDSAVEEGVTLTRFASKVTIVHRRDKLRAQSIL 185
QY 187 QDRAFNKDKIDFTWSHTTKSINEXDKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
DB 186 QARAFDNEKVDLWNTKVIKEIHENGKVGNTLVDTVTGSESEFKTDGVFIYIGMLPLSK 245
QY 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFPAAGDVDRDKLGRQIVTATGDSIAAQAAYEIE 306
DB 246 PFENLIGITNEEGYIETNDRMETKVEGIFPAAGDIREKSLRQIVTATGDSIAAQSQVHYE 305
QY 307 HLNDQARS 314
DB 306 ELQETLKT 313

RESULT 11
ADD26553
ID ADD26553 standard; protein; 315 AA.
XX
AC ADD26553;
XX
DT 15-JAN-2004 (first entry)
XX
DE B. subtilis thioredoxin reductase.
XX
KW Thioredoxin reductase; TRR; cofactor specificity;
KW computational mutagenesis; substrate specificity; PDA;
KW protein design automation; toxic protein; food allergenicity;
KW food digestibility.
XX
OS Bacillus subtilis.
XX
PN US2003100743-A1.
XX
PD 29-MAY-2003.
XX
XX 06-MAY-2002; 2002US-00141531.
XX
PF 04-MAY-2001; 2001US-0289029P.
PR 05-APR-2002; 2002US-0370609P.
PR 29-APR-2002; 2002US-0376682P.
XX
XX (DALM/) DALMIA B K.
PA (BRIG/) BRIGGS S P.
PA (VALG/) VAL G D.
PA (DEST/) DESTJALRAIS J R.
PA (HEIF/) HEIFETZ P.
PA (LUGI/) LUGINEUHL P.
PA (MUCH/) MUCHHAL U.
XX
XX Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;
PI Luginbuhl P, Muchhal U;
XX WPI; 2003-801212/75.
DR

XX
PT Altering the cofactor specificity of thioredoxin reductase, useful for
PT reducing the toxicity of toxic proteins, reducing allergenicity of food
PT and increasing the digestibility of foods, comprises computational
PT mutagenesis.
XX
XX Disclosure; Fig 21; 125pp; English.
XX
XX The invention relates to altering the cofactor specificity of thioredoxin
CC reductase (TRR) comprising computational mutagenesis. Also included are
CC altering the substrate specificity of TRR or cofactor specificity of a
CC target protein, a variant TRR protein that reduces a protein that reduces
CC a thioredoxin protein (obtained from an organism selected from
CC Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces,
CC Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused
CC to a second protein (that is either a wild-type TRR protein, thioredoxin,
CC or a variant TRR protein), producing a plant with a transformed seed of the
CC a transformed plant prepared by the method and a transformed TRR is altered
CC transformed plant. The cofactor specificity of the variant TRR is altered
CC such that the variant preferentially binds NADPH compared to NADH, or
CC vice versa. The protein design cycle comprises the sequence design algorithm,
CC (PDA (RTM)). This design cycle comprises the sequence design algorithm,
CC or a force field calculation. The variant TRR protein is fused to the
CC second protein through a linker. The variant TRR protein has 1-3 amino
CC acid substitutions as compared to the wild-type Arabidopsis TR protein.
CC The amino acid substitutions are selected from positions A4, A5 and A6,
CC preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5V, RA5Y, RA6F, RA6H,
CC RA6Q, RA6G, and RA6N. The method is useful for reducing the toxicity of
CC toxic proteins, reducing allergenicity of food and increasing the
CC digestibility of food. The invention provides an efficient and low cost
CC method as compared to prior art. The present sequence is a wild-type TRR
CC protein.
XX
XX Sequence 315 AA;
SQ

Query Match 69.4%; Score 1154; DB 7; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.5e-99;
Matches 220; Conservative 33; Mismatches 55; Indels 0; Gaps 0;
QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENPFGFEMITGPDLSL 66
DB 6 YDVIITIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENYPGFESILGPESLN 65
QY 67 KMFEHAKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKIGVPGEOE 126
DB 66 KMFEHAKFGAEYAGYDKEVIDGKEYKVKVAGSKYKARAVIIAAGAEYKKIGVPGEKE 125
QY 127 LGGRGVSYCAVCDGAFKKNKELFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
DB 126 LGGRGVSYCAVCDGAFKKGKELVVGSGDSAVEEGVTLTRFASKVTIVHRRDKLRAQSIL 185
QY 187 QDRAFNKDKIDFTWSHTTKSINEXDKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
DB 186 QARAFDNEKVDLWNTKVIKEIHENGKVGNTLVDTVTGSESEFKTDGVFIYIGMLPLSK 245
QY 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFPAAGDVDRDKLGRQIVTATGDSIAAQAAYEIE 306
DB 246 PFENLIGITNEEGYIETNDRMETKVEGIFPAAGDIREKSLRQIVTATGDSIAAQSQVHYE 305
QY 307 HLNDQARS 314
DB 306 ELQETLKT 313
RESULT 12
AAO20627
ID AAO20627 standard; protein; 315 AA.
XX
XX AAO20627;
AC
XX
XX 10-APR-2003 (first entry)
DT
XX Thioredoxin reductase variant protein sequence #26.
DE

XX Ophthalmological; virucide; vulnery; vasotropic; antiallergic;
KW cofactor specificity; thioredoxin reductase; TR; non-allergenic food;
KW computational mutagenesis; scaffold protein; oil body; animal feed;
KW digestibility; gluten; protein disulfide isomerase; PDI; enzyme;
KW scleroprotein; gelled; food; nitrosative stress response; eye disease;
KW cataract; oxidative stress; ischemic-reperfusion; acute lung injury.
XX Unidentified.
OS
XX WO200290300-A2.
PN
XX 14-NOV-2002.
XX
XX 06-MAY-2002; 2002WO-US014358.
PF
XX 04-MAY-2001; 2001US-0289029P.
PR
XX 05-APR-2002; 2002US-0370609P.
PR
XX 29-APR-2002; 2002US-00370609.
XX
XX (XENC-) XENCOR.
PA
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;
PI Luginbuhl P, Muchhal U;
XX
XX WPI; 2003-111951/10.
DR
XX
XX Altering cofactor specificity of target protein, e.g. thioredoxin
PT reductase, useful for reducing antigenicity of glutens in wheat, barley,
PT or treating disulfide linkages present in proteins, by computational
PT mutagenesis.
XX
PS Disclosure; Fig 22; 212pp; English.
XX
XX The invention relates to a novel method for altering the cofactor
CC specificity of a target protein (e.g. thioredoxin reductase (TR)) by
CC computational mutagenesis. This method involves inputting a set of
CC coordinates for a scaffold protein comprising amino acid positions,
CC applying at least one protein design cycle; and generating a set of
CC candidate variant proteins with altered cofactor specificity. The novel
CC method is useful for altering the cofactor specificity of TR scaffold
CC proteins chosen from *Escherichia coli*, *Bacillus subtilis*, *Mycobacterium*
CC *leprae*, *Saccharomyces*, *Neurospora crassa*, *Arabidopsis*, and human. Another
CC method of the invention is useful for making oil bodies which are useful
CC in the preparation of non-allergenic foods, or in the preparation of
CC animal feeds to improve the digestibility of the feeds. The variant TR
CC protein is useful for reducing the antigenicity of glutens in wheat, rye
CC or barley, to reduce alternative substrates for thioredoxin reductases,
CC including a number of plant and mammalian proteins found to contain
CC thioredoxin domains e.g. protein disulfide isomerase (PDI). The variant
CC TR protein is useful as a redox partner in compositions used for treating
CC disulfide linkages present in proteins such as enzymes, e.g., proteases,
CC amyloses, etc; and structural proteins such as scleroproteins.
CC Compositions comprising variant TR proteins and PDI are useful for
CC generating protein disulfide crosslinks yielding high molecular weight or
CC gelled compositions, and thus is useful in food processing. A further
CC method of the invention is useful for producing plants expressing variant
CC TR protein, e.g., corn and soybean provides grains with altered storage
CC protein quality as well as grains that perform qualitatively differently
CC from normal grain during industrial processing or animal digestion of
CC variant TR proteins in combination with thioredoxin, which can be used to
CC manipulate nitrosative stress, to upregulate nitrosative stress
CC responses, and thus is useful for treating eye diseases, such as
CC cataracts, where it inhibits or reverse formation of cataract in eye. The
CC variant TR protein in combination with thioredoxin is also useful for
CC minimizing oxidative stress and ischemic-reperfusion induced in acute
CC lung injury. The invention represents a thioredoxin reductase variant
CC protein of the invention
XX
XX Sequence 315 AA;
SQ

Query Match

69.3%; Score 1152; DB 6; Length 315;

Claim 82; Page 296-297; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occluding body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
XX Sequence 315 AA;

Query Match 68.9%; Score 1145.5; DB 5; Length 315;
Best Local Similarity 68.6%; Pred. No. 4.1e-98;
Matches 216; Conservative 38; Mismatches 60; Indels 1; Gaps 1;
QY 1 MGTEID-FDIAIIGAGPAGMTAAVYASRANKVTVMERIGIPGGOMANTEVENPFGPEMI 59
DB 1 MGEEQKYDVVVIAGAGPAGMTAAVYTSRANLSTVMERIGIPGGOMANTEVENPFGPDHI 60
QY 60 TGDLSLTKMEHAKKFGAAYQYGDIKSVDEKGVKINFGNKELTAKAVIATGAAYKKI 119
DB 61 LGPELSTLTKMEHAKKFGAAYAYGDIKIIDGGDLKLVKAGNKEYKARAVIATGAAYKKL 120
QY 120 GVPGEQLGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVBEGTPTTKFADKVTIVHRRDE 179
DB 121 GVPGEKLSGRGVSYCAVCDGAFFKRELVVVGSDSAVEAVYLTFRASKVTIHRDQ 180
QY 180 LRAQRIILQDRAFNKDKIDFINSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIYI 239
DB 181 LRAQKILQDRAFNKDKIEFIHVVVQKINGTDGKVSSTIEHAKTGEQQDKFTDGVFIYI 240
QY 240 GMKPLTAPFKDLGINTDVGIVTVDMMTTSVPGIPAGDVRDKGLRQIVTATGDSIAAQ 299
DB 241 GMLPNEAVKLNILNDEGIYVTNEEMETSVPGIPAGDVRDKGLRQIVTATGDSIAAQ 300
QY 300 SAAEYIEHLNDOARS 314
DB 301 NVQHYIELEAKVKN 315

RESULT 14
ADD26570 standard; protein; 309 AA.
XX ID ADD26570 standard; protein; 309 AA.
XX AC ADD26570;
XX DT 15-JAN-2004 (first entry)
XX DE B. subtilis synthetic thioredoxin reductase.
XX KW Thioredoxin reductase; TRR; cofactor specificity;
KW computational mutagenesis; substrate specificity; PDA;
KW protein design automation; toxic protein; food allergenicity;
KW food digestibility; mutant; muten.
XX OS Synthetic.
OS Bacillus subtilis.
XX US2003100743-A1.
XX 29-MAY-2003.

PF 06-MAY-2002; 2002US-00141531.
XX
XX 04-MAY-2001; 2001US-0289029P.
PR 05-APR-2002; 2002US-0370609P.
PR 29-APR-2002; 2002US-0376682P.
XX
XX (DALM/) DALMIA B K.
PA (BRIG/) BRIGGS S P.
PA (VALG/) VAL G D.
PA (DESG/) DESJARLAIS J R.
PA (HEIF/) HEIFETZ P.
PA (LUGI/) LUGINBUHL P.
PA (MUCH/) MUCHHAL U.
XX
XX Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;
PI Luginbuhl P, Muchhal U;
PI
XX MPI; 2003-801212/75.
XX
XX Altering the cofactor specificity of thioredoxin reductase, useful for
PT reducing the toxicity of toxic proteins, reducing allergenicity of food
PT and increasing the digestibility of foods, comprises computational
PT mutagenesis.
XX
XX Claim 30; Page; 125pp; English.
XX
XX The invention relates to altering the cofactor specificity of thioredoxin
CC reductase (TRR) comprising computational mutagenesis. Also included are
CC altering the substrate specificity of TRR or cofactor specificity of a
CC target protein, a variant TRR protein that reduces a protein that reduces
CC a thioredoxin protein (obtained from an organism selected from
CC Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces,
CC Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused
CC to a second protein (that is either a wild-type TRR protein, thioredoxin,
CC or a variant TRR protein), producing a plant with a modified TRR protein,
CC a transformed plant prepared by the method and a transformed seed of the
CC transformed plant. The cofactor specificity of the variant TRR is altered
CC such that the variant preferentially binds NADPH compared to NADH, or
CC vice versa. The protein design cycle comprises protein design automation
CC (PDA (RTM)). This design cycle comprises the sequence design algorithm,
CC or a force field calculation. The variant TRR protein is fused to the
CC second protein through a linker. The variant TRR protein has 1-3 amino
CC acid substitutions as compared to the wild-type Arabidopsis TR protein.
CC The amino acid substitutions are selected from positions A4, A5 and A6,
CC preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5V, RA6Y, RA6I, RA6L,
CC RA6Q, RA6G, and RAGN. The method is useful for reducing the toxicity of
CC toxic proteins, reducing allergenicity of food and increasing the
CC digestibility of food. The invention provides an efficient and low cost
CC method as compared to prior art. The present sequence is a synthetic
CC thioredoxin reductase comprising ligated functional fragments of a wild-
XX type TRR protein.

XX Sequence 309 AA;
SQ
Query Match 65.6%; Score 1090; DB 7; Length 309;
Best Local Similarity 69.5%; Pred. No. 5.9e-93;
Matches 214; Conservative 33; Mismatches 55; Indels 6; Gaps 3;
QY 7 FDIAIIGAGPAGMTAAVYASRANKVTVMERIGIPGGOMANTEVENPFGPEMIGPDLST 66
DB 6 YDVIIIGAGPAGMTAAVYTSRANLSTLMEIRIGIPGGOMANTEVENPFGPESILGPESLN 65
QY 67 KMFEHAKKFGAAYQYGDIKSVDEKGVKINFGNKELTAKAVIATGAAYKKIYGVGQOE 126
DB 66 KMFEHAKKFGAAYAYGDIKEVIDGKEYKVKVAGSKYKARAVIIAAGAYKKIYGVGQOE 125
QY 127 LGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEGCTFTTKFADKVTIVHRRDELRAQRI 186
DB 126 LGGRGVSYCAVCDGAFFKRELVVVGSD--VEEGVYLTFRASKVTIV--DKL-AQSLL 179
QY 187 QDRAFNKDKIDFINSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
DB 180 QARAFDNKVDLWNTKVIHEENGKVGNTVLDVTVTGSESEFKTDGTVFIYIGMLPLSK 239

187 QDRAFNKDIDFIWSHTTTSINEKDGKGVSLTSTXKDSEETHEADGVFIYIGMKPLTA 246

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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:13:58 ; Search time 40 Seconds
(without alignments)
769.532 Million cell updates/sec

Title: US-09-825-212-1
Perfect score: 1662
Sequence: 1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1562	95.2	311	2 E89849	thioredoxine reduct
2	1157	69.6	316	1 A69727	thioredoxin-disulf
3	1145.5	68.9	315	2 C84096	thioredoxin reduct
4	1057	63.6	319	2 AH1759	thioredoxin reduct
5	1054	63.4	319	2 AFI384	thioredoxin reduct
6	872	52.5	308	2 D86742	thioredoxin-disulf
7	851	51.2	303	2 G98035	thioredoxin-disulf
8	849	51.1	303	2 G95169	thioredoxin reduct
9	728.5	43.8	325	2 A75330	thioredoxin reduct
10	726	43.7	315	1 D35156	thioredoxin-disulf
11	706	42.5	315	1 S63990	thioredoxin-disulf
12	697.5	42.0	307	2 C71278	thioredoxin reduct
13	687	41.3	317	2 H72322	thioredoxin reduct
14	671	40.4	308	2 B97007	thioredoxin-disulf
15	668	40.2	308	1 S23117	probable thioredox
16	645.5	38.8	345	2 D75116	thioredoxin reduct
17	644.5	38.8	322	1 A53307	thioredoxin-disulf
18	643.5	38.7	336	2 D71016	thioredoxin reduct
19	641.5	38.6	310	2 B97777	thioredoxin-disulf
20	639.5	38.5	335	1 S70851	thioredoxin-disulf
21	632.5	38.1	458	1 S77662	probable trxB2 pro
22	626.5	37.7	322	2 T36577	thioredoxin reduct
23	619.5	37.3	310	2 D71703	thioredoxin reduct
24	605	36.4	351	2 B71556	probable thioredox
25	601	36.2	318	1 G64186	thioredoxin-disulf
26	599.5	36.1	303	1 E69194	thioredoxin-disulf
27	598.5	36.0	333	2 T41743	thioredoxin-disulf
28	595	35.8	311	2 B86530	thioredoxin reduct
29	595	35.8	311	2 C72093	thioredoxin reduct

30	593	35.7	312	2 C81710	thioredoxin reduct
31	591.5	35.6	483	2 AG1898	thioredoxin reduct
32	587.5	35.3	320	2 T42062	thioredoxin-disulf
33	584.5	35.2	535	2 T00824	probable thioredox
34	584	35.1	348	2 G87604	thioredoxin reduct
35	581.5	35.0	383	2 A84552	probable thioredox
36	579.5	34.9	333	1 S44027	thioredoxin-disulf
37	575	34.6	300	1 A69444	thioredoxin-disulf
38	573.5	34.5	320	2 AH0167	thioredoxin-disulf
39	570.5	34.3	362	2 D84281	thioredoxin limpor
40	569.5	34.3	321	1 RDECT	thioredoxin-disulf
41	569.5	34.3	321	2 E90750	thioredoxin reduct
42	569.5	34.3	321	2 C85614	thioredoxin reduct
43	564	33.9	307	2 A99601	thioredoxin reduct
44	563.5	33.9	322	2 AD0611	thioredoxin reduct
45	563	33.9	328	2 AF2081	thioredoxin reduct

ALIGNMENTS

RESULT 1
E89849
thioredoxine reductase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: E89849
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaico, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700655; PIDN:BA841952.1; GSPDB:GN00149
C:Experimental source: strain N315
C:Genetics:
A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 95.2%; Score 1582; DB 2; Length 311;
Best Local Similarity 99.4%; Pred. No. 2.9e-111;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	3	TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVEVFPFEMITGP	62
Db	2	TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVEVFPFEMITGP	61
QY	63	DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAEYKKGVP	122
Db	62	DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAEYKKGVP	121
QY	123	GEQELGGRGVSCAVCDGAFKFKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA	182
Db	122	GEQELGGRGVSCAVCDGAFKFKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA	181
QY	183	QRILQDRAFKNDKIDFIWSHTTKSINEKDGKGVSTLTSTKDGSEETHEADGVFIYIGMK	242
Db	182	QRILQDRAFKNDKIDFIWSHTTKSINEKDGKGVSTLTSTKDGSEETHEADGVFIYIGMK	241
QY	243	PLTAPFKDLGINTDVGIVTVDKMTTTSVPGIFAAGDVEDKGLRQIVTATGSGTAQAASAA	302
Db	242	PLTAPFKDLGINTDVGIVTVDKMTTTSVPGIFAAGDVEDKGLRQIVTATGSGTAQAASAA	301
QY	303	EYIEHLNDQA 312	
Db	302	EYIEHLNDQA 311	

RESULT 2

Wed Sep 15 13:38:57 2004

A69727
C:Species: Bacillus subtilis
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
C:Accession: A69727
R:Kunz, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Brouillet, S.; Bruchet, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chhabra, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallon, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, A.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaite, Y.; Sato, T.; Scanlon, A.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69727
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-316 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:92635827; PIDN:CAB15484.1; PID:92635992
A:Experimental source: strain 168
C:Genetics:
A:Gene: trxB
C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
C:Function:
A:Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide
F:3-305/Domain: thioredoxin reductase homology <TRXB>
F:8-36/Region: beta-alpha-beta FAD nucleotide-binding fold
F:147-174/Region: beta-alpha-beta NADP nucleotide-binding fold
F:135-138/Disulfide bonds: redox-active #status predicted

Query Match 69.6%; Score 1157; DB 1; Length 316;
Best Local Similarity 70.7%; Pred. No. 2.2e-79;
Matches 222; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLTKVMIERGIPGGQMANTEVENFPGFEMI 60
Db 1 MSEKIDYDVIIIGAGPAGMTAAVYTSRANLTKVMIERGIPGGQMANTEVENFPGFEMI 60

Qy 61 GPDLSTKMFHAKKFGAVYQYGDIVKSVEDKGYKVINFGNKELTAKAVIIATGAEYKKIG 120
Db 61 GPDLSTKMFHAKKFGAVYQYGDIVKSVEDKGYKVINFGNKELTAKAVIIATGAEYKKIG 120

Qy 121 VPGQELGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 180
Db 121 VPGQELGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 180

Qy 181 RAQRIQLQDRAFNKIDFINSHTTKSINEKDGKGVSVTLSTKDGSEETHEADGVFIYI 240
Db 181 RAQRIQLQDRAFNKIDFINSHTTKSINEKDGKGVSVTLSTKDGSEETHEADGVFIYI 240

Qy 241 VPGQELGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 300
Db 241 VPGQELGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 300

Qy 301 AAEYIEHLNDQARS 314
Db 301 VQHYVEELQETLTK 314

RESULT 3
C84096
thioredoxin reductase (NADPH) trxB [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: C84096
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirata, Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20512582; PMID:11059132
A:Accession: C84096
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:G10176109; PIDN:BA07290.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 68.9%; Score 1145.5; DB 2; Length 315;
Best Local Similarity 68.8%; Pred. No. 1.1e-78;
Matches 216; Conservative 38; Mismatches 60; Indels 1; Gaps 1;

Qy 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLTKVMIERGIPGGQMANTEVENFPGFEMI 59
Db 1 MGTEIDFDIAIIGAGPAGMTAAVYTSRANLTKVMIERGIPGGQMANTEVENFPGFEMI 60

Qy 60 TGPDLSTKMFHAKKFGAVYQYGDIVKSVEDKGYKVINFGNKELTAKAVIIATGAEYKKI 119
Db 60 TGPDLSTKMFHAKKFGAVYQYGDIVKSVEDKGYKVINFGNKELTAKAVIIATGAEYKKI 120

Qy 120 VPGQELGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDE 179
Db 120 VPGQELGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDE 180

Qy 180 LRAQRIQLQDRAFNKIDFINSHTTKSINEKDGKGVSVTLSTKDGSEETHEADGVFIYI 239
Db 180 LRAQRIQLQDRAFNKIDFINSHTTKSINEKDGKGVSVTLSTKDGSEETHEADGVFIYI 240

Qy 240 GMKPLTAPFKDLGITNDVGVIIKDDMTTSVPGIFANGDVDRKGLRQIVTATGDSIAAQ 299
Db 240 GMKPLTAPFKDLGITNDVGVIIKDDMTTSVPGIFANGDVDRKGLRQIVTATGDSIAAQ 300

Qy 300 SAAEYIEHLNDQARS 314
Db 301 NVQHYVEELAEKVKVN 315

RESULT 4
AH1759
thioredoxin reductase [imported] - Listeria innocua (strain Clipl1262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1759
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1759
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97848.1; PID:G16415158; GSPDB:GN00178
A:Experimental source: strain Clipl1262
C:Genetics:
A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 63.6%; Score 1057; DB 2; Length 319;
Best Local Similarity 65.8%; Pred. No. 7e-72;
Matches 200; Conservative 44; Mismatches 60; Indels 0; Gaps 0;

Qy 7 FDIAIIGAGPAGMTAAVYASRANLTKVMIERGIPGGQMANTEVENFPGFEMITGPDLS 66

Db 8 YDVIIGAGPAGMTAAALYTSRADLDTLMIERGVPGQWNTAEVENVPGFDSILGPDLS 67
 QY 67 KMFEHAKFGAVYQYGDVSKVEDKGYKVINFGNKLTAQAVIIATGAYKKIGVPGQEE 126
 Db 68 KMLSGAKQFGAYAYGDIKEVDGKEFTVITAGSKTYKARAIITATGAHRKLGAAEGEE 127
 QY 127 LGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 186
 Db 128 LSGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 187
 QY 187 QDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMKPLTA 246
 Db 188 QDRAFKDEKVDFIWNTVEEIIIGDGKKVTSVKLVSTVDGSESIMPVDGVFIYVGLVPLTK 247
 QY 247 PFKDLGITNDVGYITVKDDMTTSVPGIIFAAAGDVDRKGLRQIVTATGSGSIAAQAAYIE 306
 Db 248 AFLNLGITDDEGIYVTDDEMRNLPGIIFAAAGDVRAKSLRQIVTATGSGGLAGQNAQKYVE 307
 QY 307 HLND 310
 Db 308 ELKE 311

RESULT 5

AF1384
 thioeredoxin reductase [imported] - Listeria monocytogenes (strain EGD-e)
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C;Accession: AF1384
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001
 A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AF1384
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-319 <GLA>
 A;Cross-references: GB:NC_003210; PIDN:CAD00556.1; PID:gi6411966; GSPDB:GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: trxB
 C;Superfamily: thioeredoxin reductase; thioeredoxin reductase homology

Query Match 63.4%; Score 1054; DB 2; Length 319;
 Best Local Similarity 65.5%; Pred. No. 1.2e-71;
 Matches 199; Conservative 43; Mismatches 62; Indels 0; Gaps 0;

QY 7 FDIAGAGPAGMTAAVYASRANLKTVMIERGIPGQMANTAEVENPFGFEMITGPDIST 66
 Db 8 YDVIIGAGPAGMTAAALYTSRADLDTLMIERGVPGQWNTAEVENVPGFDSILGPDLS 67
 QY 67 KMFEHAKFGAVYQYGDVSKVEDKGYKVINFGNKLTAQAVIIATGAYKKIGVPGQEE 126
 Db 68 KMLSGAKQFGAYAYGDIKEVDGKEFTVITAGSKTYKARAIITATGAHRKLGAAEGEE 127
 QY 127 LGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 186
 Db 128 LSGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 187
 QY 187 QDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMKPLTA 246
 Db 188 QDRAFKDEKVDFIWNTVEEIIIGDGKKVTSVKLVSTVDGSESIMPVDGVFIYVGLVPLTK 247
 QY 247 PFKDLGITNDVGYITVKDDMTTSVPGIIFAAAGDVDRKGLRQIVTATGSGSIAAQAAYIE 306
 Db 248 AFLNLGITDDEGIYVTDDEMRNLPGIIFAAAGDVRAKSLRQIVTATGSGGLAGQNAQKYVE 307
 QY 307 HLND 310

Db 308 ELKE 311

RESULT 6

D86742
 thioeredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Lactococcus lactis subsp. lac.
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Jun-2002
 C;Accession: D86742
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich, Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s.
 A;Reference number: AB6625; MUID:21235186; PMID:11337471
 A;Accession: D86742
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <STO>
 A;Cross-references: GB:AE005176; PID:gl2723976; PIDN:AAK05038.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: trxB1
 C;Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 C;Keywords: oxidoreductase

Query Match 52.5%; Score 872; DB 2; Length 308;
 Best Local Similarity 53.1%; Pred. No. 5e-58;
 Matches 163; Conservative 54; Mismatches 90; Indels 0; Gaps 0;

QY 3 TEIDFDIAIAGPAGMTAAVYASRANLKTVMIERGIPGQMANTAEVENPFGFEMITGP 62
 Db 2 TEKYDVIIIGSGPAGMTAAVYASRANLKTVMIERGIPGQMANTAEVENPFGFEMITGP 61
 QY 63 DLSTKMFHAKFGAVYQYGDVSKVEDKGYKVINFGNKLTAQAVIIATGAYKKIGVP 122
 Db 62 ELSMKMAEPLEGIVENAGVTAIEDHGYKKIITDEDFVTKSIIIIATGANHRKLETP 121
 QY 123 GRQELGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRA 182
 Db 122 GEEYGARGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRA 181
 QY 183 QRILQDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMK 242
 Db 182 QELIQDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMK 241
 QY 243 PLTAPFKDITNDVGYITVKDDMTTSVPGIIFAAAGDVDRKGLRQIVTATGSGSIAAQA 302
 Db 242 PVAEFAGNLGITDEAGWIITDHDHMTSLPGIPAVGDRKQKDFRQITTAIGDGAQAQAEAY 301
 QY 303 EYIEHLN 309
 Db 302 KFVAELD 308

RESULT 7

G98035
 thioeredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae (stra
 C;Species: Streptococcus pneumoniae
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
 C;Accession: G98035
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeGoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234
 A;Accession: G98035
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-303 <KUR>
 A;Cross-references: GB:AE007317; PIDN:AAL00116.1; PID:gl5458956; GSPDB:GN00174
 C;Genetics:

A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
C:Keywords: oxidoreductase

Query Match	51.2%	Score	851;	DB	2;	Length	303;
Best Local Similarity	54.0%;	Pred. No.	1.9e-56;				
Matches	163;	Conservative	55;	Mismatches	82;	Indels	2;
Gaps							
Qy	7	FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENPGFEMITGPOLST	66				
Db	2	YDTIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMNTSDIENTPGYANISGPALAE	61				
Qy	67	KMFPEHAKKFGAVYQYGDIKSYEDKRGYKVINFGNKELTAKAVIIATGAEYKKIGVPGSEQ	126				
Db	62	KMFPELENLGVHEHYGVYVENVEDHGDPKVMVTDQTYETRTVIVATGSKHRPLGVPVGGEE	121				
Qy	127	LGGRGVSYCAVCDGAGFFKNNKELFVILGGDSAVESGTFPTTKADKVTIVHRRDELRACORIL	186				
Db	122	LNSRGVSYCAVCDGAGFFRDQLLVVGGDSAVEEALFLTRFAKVTIVHRRDQLRQAQKVL	181				
Qy	187	QDRAFKNDKIDFIWSHTTKTSINEKDGKGVSVTLTSTKDGSBETHEADGVFIYIGMKPLTA	246				
Db	182	QDRAFANEKISFIWDSVVKEL-KGENRVSVVFNKVTQVTEQAFGGVFVVLGDLPLSD	240				
Qy	247	PFKDLGINDVGYIVTKDDMTTSVPGIIFAGDVDRDKGLRQIVTATGDGSIQAQSAEYI-	305				
Db	241	FVKELNIQDQAGWIVTDSHMKTAVDGI FAVGVDRLKDLRQVTTAVDGDGAIAGQEA YKFI	300				
Qy	306	EH	307				
Db	301	EH	302				

RESULT 8

G95169
thioredoxin reductase [imported] - Streptococcus pneumoniae (strain TIGR4)
C1:Species: Streptococcus pneumoniae
C1>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C1:Accession: G95169
R1:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A1:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A1:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A1:Reference number: A95000; MUID:21357209; PMID:11463916
A1:Accession: G95169
A1>Status: preliminary
A1:Molecule type: DNA
A1:Residues: 1-303 <KUR>
A1:Cross-references: GB:AE005672; PIDN:AAK75552.1; PID:gi4972947; GSPDB:GN00164; TIGR:SP04
A1:Experimental source: strain TIGR4

C; Gene: SP1458
C; Superfamily: thioredoxin reductase; thioredoxin reductase homology

[illegible]

```

Db      182 QDRAFANEKISFIWDSVVREI - KGENRVESVVFENVKTQVTQQAFCGVFIYVGDLPLSD 240
        ||||| :||| ||| : | : | ||| : | | ||||| :| : |||
Qy      247 PKFDLGTINDVCYIVITKDMMTSPGIFAAAGDVNRDKGLRQLIVTATGDGSTAAQSAAEYI - 305
        ||||| :||| ||| : | : | ||| : | | ||||| :| : |||
Db      241 FVKELNIQDQAGWIYTDNHEMTAVDGFVAGDVRLKDLRQVTTAVGDGAIAGEAYKFIT 300
        ||||| :||| ||| : | : | ||| : | | ||||| :| : |||
Qy      306 EH 307
        ||
Db      301 EH 302
        ||

RESULT 9
A75330
thioredoxin reductase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75330
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodd,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
```

RESULT 9

A75330
thioredoxin reductase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75330
R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999.
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75330
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <WHI>
A:Cross-references: GB:AE02036; GB:AE000513; NID:G6459766; PIDN:AAF11534.1; PID:G6459766
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1982
A:Map position: 1
C:Classification: thioredoxin reductase; thioredoxin reductase homology

```

Query Match      43.8%; Score 728.5; DB 2; Length 325;
Best Local Similarity 48.4%; Pred. No. 3.1e-47;
Matches 152; Conservative 51; Mismatches 100; Indels 11; Gaps 4

QY      3 TEIDFDIAIIGAGPAGMTAAVYASRANKLTKVMIERGIPGGOMANTEEVNPGF-EMITG 61
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      5 TAHDVDVVIIGGPAGLTAAYITGQAQLSTLILEKMPGGQIAWSEVENFGFPPIAG 64
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      62 POLSTKMFETHAKKFGAVQYGDIKSVEDKGEYKVINFG-----NKLTAKAVIATCAEYK 117
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      65 MELAQRMHQQAEEKFAGKAVEMDEVGQYQHDATSHYPFTVRYNGEYRAKAVIATGADPR 124
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      118 KIGVPGEOELGGRGVSYCAVCDGAPFKNRLFVIGGDSAVEEGTPTTKFADKVTIVHRR 177
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      125 KIGIPGDDNFWKGVGSTCATCGDGFYKGVKVVVIGGDAARVEEGMFLTKFADEVTVIHR 184
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      178 DELRAQRIQLQDRAFNKDKIDFIWSHTTKSINKEKDGKGVSTLTSTKDGSEETHEADGVFI 237
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      185 DTLRANKVAQARAFAFANPKMKFIWDTAVEEIQAD-SVSGVKLRNLKLTGEVSELATDGVFI 243
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      238 YIGMKPLTAPFDLGLITNDVGIVYTKDDMTTSVPGIFAAQGDVRDKGLRQIVTATGDSIA 297
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      244 FIGHVNTAFVKDVTSLRDGVDYVERDEIYTNPLFAAGDVS DYIRQLATS VGAGTRA 303
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      298 A-----QSAAEYIE 306
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :
QY      304 AMTERQLAALEVE 317
Db      1 - - - - - : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
D35156
thioredoxin-disulfide reductase (EC 1.8.1.9) - Eubacterium acidaminophilum
N;Alternate names: dihydrolipoamide dehydrogenase [misidentification]
C;Species: Eubacterium acidaminophilum
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
C;Accession: S38988; D35156
R;Luebbers, M.; Andreesen, J.R.
Eur. J. Biochem. 217, 791-798, 1993

```

RESULT 10

D35156
thioredoxin-disulfide reductase (EC 1.8.1.9) - Eubacterium acidaminophilum
N:Alternate names: dihydropolipamide dehydrogenase [misidentification]
C:Species: Eubacterium acidaminophilum
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
C:Accession: S38983; D35156
R:Luebers, M.; Andreesen, J.R.
Eur. J. Biochem. 217, 791-798, 1993

A:Title: Components of glycine reductase from *Eubacterium acidaminophilum*. Cloning, sequ
 A:Reference number: S3988; MUID:94039119; PMID:8223622
 A:Accession: S3988
 A:Molecule type: DNA
 A:Residues: 1-315 <LNE>
 A:Cross-references: GB:L04500; NID:g2708733
 R:Dietrichs, D.; Meyer, M.; Schmidt, B.; Andreesen, J.R.
 J. Bacteriol. 172, 2088-2095, 1990
 A:Title: Purification of NADPH-dependent electron-transferring flavoproteins and N-termi
 A:Reference number: A35156; MUID:90202731; PMID:2318809
 A:Accession: D35156
 A:Molecule type: protein
 A:Residues: 1-33, 'X', 35-46, 'X', 48, 'D', 50-55 <DIE>
 A:Note: the designation "atypically small dihydrolipoamide dehydrogenase" was revised in
 C:Genetics:
 A:Gene: trxB
 A:Start codon: GTG
 C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
 C:Function:
 A:Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH
 C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
 C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide
 F:1-309/Domain: thioredoxin reductase homology <TRXB>
 F:6-34/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:146-173/Region: beta-alpha-beta NADP nucleotide-binding fold
 F:134-137/Disulfide bonds: redox-active #status predicted
 Query Match 43.7%; Score 726; DB 1; Length 315;
 Best Local Similarity 49.8%; Pred. No. 4.6e-47;
 Matches 153; Conservative 50; Mismatches 96; Indels 8; Gaps 3;
 QY 7 FDIATIGAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEEVENPPG-FEMITGPDLS 65
 Db 5 YDLAIIGSGPAGLAALYARAKMTIMIEGQKVGQIVITHEVANYPGSVREATGPSLI 64
 QY 66 TKMFEHAKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIATGAEYKKGIVPGSQ 125
 Db 65 ERMEEQANFGEAKVMDKIVDVLQDKIKVIGKEAEYKAKSVILATGAAPRLAGCPGQ 124
 QY 126 ELGGRGVSYCAVCDGAFKFKKRLFVIGGDSVAEEGTFTTKADKVTIVHRRDELRAQRI 185
 Db 125 ELTGKGVSYCATCDADFFEDMEVFVGGDTAVEEAMYLAKFARKVTIVHRRDELRAAKS 184
 QY 186 LQDRAFKNDKIDPIHSHHTKTSINEKDKGVGS-----VLTSTKDGSEETHEADGVFIYI 239
 Db 185 IQEKAFKPKLDPMNMSALEEI-KGDGIVESAVFKNLVTGETEYFANEEDGTGFIYFI 243
 QY 240 GMKPLTAPKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVROKGLRQIVTATGDSIAAQ 299
 Db 244 GYIPKSDVFKGKITLDDAGYIITDDNMKTNVDGVFAAGDIRVKSRLQVVVTACADGAIAAT 303
 QY 300 SAAEYIE 306
 Db 304 QAEKYVE 310
 RESULT 11
 S63990
 N:Alternate names: glycine reductase complex Clostridium litorale
 C:Species: Clostridium litorale
 C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
 R:Kreimer, S.; Andreesen, J.R.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: S63990
 A:Accession: S63990
 A:Molecule type: DNA
 A:Residues: 1-315 <KRE>
 A:Cross-references: EMBL:U24268; NID:g1171124; PIDN:AAC43575.1; PID:g1171125
 R:Kreimer, S.; Andreesen, J.R.
 Eur. J. Biochem. 234, 192-199, 1995
 A:Title: Glycine reductase of *Clostridium litorale*. Cloning, sequencing, and molecular a

A:Reference number: S63987; MUID:96096738; PMID:8529640
 A:Accession: S63987
 A:Molecule type: DNA
 A:Residues: 1-117 <XRW>
 A:Cross-references: EMBL:U24268; NID:g1171124
 C:Genetics:
 A:Gene: trxB
 A:Start codon: GTG
 C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
 C:Function:

A:Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH
 C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
 C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide
 F:1-309/Domain: thioredoxin reductase homology <TRXB>
 F:6-34/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:146-173/Region: beta-alpha-beta NADP nucleotide-binding fold
 F:134-137/Disulfide bonds: redox-active #status predicted

Query Match 42.5%; Score 706; DB 1; Length 315;
 Best Local Similarity 48.5%; Pred. No. 1.5e-45;
 Matches 150; Conservative 53; Mismatches 98; Indels 8; Gaps 3;
 QY 7 FDIATIGAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEEVENPPG-FEMITGPDLS 65
 Db 5 YDLAIIGSGPAGLAALYARAKMTLLLEGKVGQIVITHEVANYPGSVPEATGPSLI 64
 QY 66 TKMFEHAKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIATGAEYKKGIVPGSQ 125
 Db 65 GRMEEQVEFGAERVMDNIVDFTDKIKVIGKEAEYKAKAVIATGASPKIAGCPGEK 124
 QY 126 ELGGRGVSYCAVCDGAFKFKKRLFVIGGDSVAEEGTFTTKADKVTIVHRRDELRAQRI 185
 Db 125 ELTGKGVSYCATCDADFFEDMEVFVGGDTAVEEAMLTKEFARKVTIVHRRDELRAAKS 184
 QY 186 LQDRAFKNDKIDPIHSHHTKTSINEKDKGVGSVLTSTKDG-----SEETHEADGVFIYI 239
 Db 185 IQEKAFKPKLDPMNMTVIEEI-KGDGIVESAVFKNRETGEVTEFVAPEEDGTGFIYFI 243
 QY 240 GMKPLTAPKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVROKGLRQIVTATGDSIAAQ 299
 Db 244 GYDPKLSALVEGKLELDETGYIPTDDNMKTNVEGVFAAGDIRVKSRLQVVVTATADGAIAAV 303
 QY 300 SAAEYIEHL 308
 Db 304 QAEKYIEEL 312

RESULT 12

C71278

probable thioredoxin reductase (trxB) - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

C:Accession: C71278

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDO

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: C71278

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-307 <COL>

A:Cross-references: GB:AE001252; GB:AE000520; NID:g3323119; PIDN:AAC65780.1; PID:g332312

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0814

C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

F:1-302/Domain: thioredoxin reductase homology <TRXB>

Query Match

Best Local Similarity 42.0%; Score 697.5; DB 2; Length 307;

Matches 142; Conservative 55; Mismatches 108; Indels 3; Gaps 3;

QY 4 EIDEDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVENFPGFEM-ITGP 62
 DB 2 ETDYDVIIVGAGAGLSAAQYACRANLRTLVIESAHGQALLIDSLNPGYATPISGF 61
 QY 63 DLSTKMFHAKFGAVYQYD1KSVDEKGEYKVINFGNKELTAKAVIATGAEYKIGVP 122
 DB 62 EYAEENMKQAVAFGAQIAVEEVTTIGKRSVSFHTTGTGAYTAMSVILATGAHRKMGIP 121
 QY 123 GSOELGGRGVSYCAVCDGAGFFKNKRLFTVIGGDSAVEEGTFTTKPADKVTIVHRRDELRA 182
 DB 122 GESEFLGRGVSYCATCDGPFPRNKHVVVIGGGDAACDESILVSLRLTRDVTMHRDLRA 181
 QY 183 ORLQDRAFNKDKIDFIWHSHTTKSINEXDKGVSFTLTSTKDGSEETHADGVFIYGMK 242
 DB 182 QKAIARTLKNPHIAVQWNTLTLEAV-RGETKVSSVLLKDVKTGETRELACDAVFFFIGMV 240
 QY 243 PLTAPFKDLGITNDVGVIVTKDDMTTSVPOIFPAAGDVRDKGLRQIVTATGDSIAQSA 302
 DB 241 PITGLLPD-AEKDSTGYIVTDDMTTSVEGIFPAAGDVRKAKSFRQVITATSDGALAHA 299
 QY 303 EYIEHLND 310
 DB 300 SYIDTLQN 307

RESULT 13
 H72322
 thioeredoxin reductase - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: H72322
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; PMID:99287316; PMID:10360571
 A:Accession: H72322
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <ARN>
 A:Cross-references: GB:AE001753; GB:AE000512; NID:G4981397; PIDN:AA035951.1; PID:G498140
 A:Experimental source: strain MSB8
 C:Genetics:
 C:Gene: TM0869
 C:Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 F:14-316/Domain: thioeredoxin reductase homology <TRXB>

Query Match 41.3%; Score 687; DB 2; Length 317;
 Best Local Similarity 44.8%; Pred. No. 3.9e-44;
 Matches 134; Conservative 63; Mismatches 100; Indels 2; Gaps 2;
 QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVENFPGFEMITGPDLST 66
 DB 18 YDIVVVGPGAGLSAIVARRAGLSVLVVEKAIEGGYVNLTHLVENPFGFPAISGEELAS 77
 QY 67 KMFEHAKFGAVYQYD1KSVDEKGEYKVINFGN-KELTAKAVIATGAEYKIGVPGRQ 125
 DB 78 KPEHAERKFGADIVNVEVVKLVQGGDKVVDLDDGKRLEAPVIVVATGANPKLVNVEGK 137
 QY 126 ELGGRGVSYCAVCDGAGFFKNKRLFTVIGGDSAVEEGTFTTKPADKVTIVHRRDELRAQRI 185
 DB 138 EFPFGKGVSYCATCDGLYFAGKDVIVVGGDSACDESIFLSNIVNKITMIQLLETLLAAKY 197
 QY 186 LQDRAFNKDKIDFIWHSHTTKSINEXDKGVSFTLTSTKDGSEETHADGVFIYGMKPLT 245
 DB 198 LQERVLNPKIEVYNSVREIRGKD-KVEEVVIVNKTGETKVLKADGVFIIGLDPS 256
 QY 246 APFKDLGITNDVGVIVTKDDMTTSVFGIFPAAGDVRDKGLRQIVTATGDSIAQSAAY 304
 DB 257 KLEGLVELDPYGVIVTDENNETSVKGIYAVGVRKKNLRFQIVTAVADGAIAVEHAHAK 315

RESULT 14
 B97007
 thioeredoxine reductase [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: B97007
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; PMID:21359325; PMID:21359325
 A:Accession: B97007
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-308 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK78845.1; PID:G15023764; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 C:Gene: CAC0869
 C:Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 Query Match 40.4%; Score 671; DB 2; Length 308;
 Best Local Similarity 42.2%; Pred. No. 6e-43;
 Matches 130; Conservative 74; Mismatches 102; Indels 2; Gaps 2;
 QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVENFPGPEMIT 60
 DB 1 MKKEKILDLVILGAGPAGLTAGIYSSRAKLDFIILENLVGGQIRETPSIENPGFDSIS 60
 QY 61 GPDLSTKMFHAKFGAVY-QYD1KSVDEKGEYKVINFGNKELTAKAVIATGAEYKVI 119
 DB 61 GADLADKQWEHAEKAGAVIDEFGNITSVKLTDEKIFETSDTIYKPKSVIATGSKRPL 120
 QY 120 GVPGEQLGGRGVSYCAVCDGAGFFKNKRLFTVIGGDSAVEEGTFTTKPADKVTIVHRRDE 179
 DB 121 VPVEKKLRGKGIHICELCDGAMVDGKDIVVVGGSNAIDAAIPLTKYAKNLTVVHRSEK 180
 QY 180 LRAQRIILQDRAFNKDKIDFIWHSHTTKSINEXDKGVSFTLTSTKDGSEETHADGVFIYI 239
 DB 181 LRAEMRSQDELFKNNVKKLLNLTQIKHV-EGENSIENIVLENSKTGKSLKADAIFYI 239
 QY 240 GMKELTAPFKDLGITNDVGVIVTKDDMTTSVFGIFPAAGDVRDKGLRQIVTATGDSIAAQ 299
 DB 240 GTMPEKTELKFDIDLTELGHKINENLETNIKGVFAAGDVRKREIQLTAVNDGSIASL 299
 QY 300 SAABYIEH 307
 DB 300 MAEKYIRN 307

RESULT 15
 S29117
 thioeredoxin-disulfide reductase (EC 1.8.1.9) - Clostridium pasteurianum
 C:Species: Clostridium pasteurianum
 C>Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
 C:Accession: S29117
 R:Mathieu, I.; Meyer, J.; Moulis, J.M.
 Biochem. J. 285, 255-262, 1992
 A:Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin gene
 A:Reference number: S29117; PMID:92344580; PMID:1637309
 A:Accession: S29117
 A:Molecule type: DNA
 A:Residues: 1-308 <MAT>
 A:Cross-references: EMBL:M60116; NID:G144905; PIDN:AAA23276.1; PID:G144906
 C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
 C:Function:
 A:Description: catalyzes the reversible reduction of oxidized thioeredoxin by NADPH
 C:Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide
 F:3-305/Domain: thioeredoxin reductase homology <TRXB>
 F:8-36/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:148-175/Region: beta-alpha-beta NADP nucleotide-binding fold

F:136-139/Disulfide bonds: redox-active #status predicted

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Query Match      40.2%; Score 668; DB 1; Length 308;
Best Local Similarity 43.8%; Pred. No. 1e-42;
Matches 134; Conservative 64; Mismatches 106; Indels 2; Gaps 2;

QY      1 MGTEIDFDIALIGAPAGMTAAVYASRANLKTVMIERGIPGQOMANTEEVENFPFGFEMIT 60
Db      1 MKEEKQLDLVLIIGAGPAGLTAAYAIRAKLNTLVLENELVGGQIRETYTVENFPFGFVIS 60

QY      61 GPDLSKWEHEHAKKFGA-VVOYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKXI 119
Db      61 GADLADKWEHEHAAISIGNIDQFSNIEKIKLSDDEKIIETEDVIYKVKALIIATCAKGRRL 120

QY      120 GVPGEQLGGRGVSYCAVCDGAPFKNRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDE 179
Db      121 PIPPEEKLGKVIHYCELCDGALYQGRDLVVVGGGNSAVEAAFLTXYARNITIVHQFDY 180

QY      180 LRAQRILQDRAFKNDKIDFTWSHTTKSINEKDGKVGSVTLTSTKOGSEETHEADGVFIYI 239
Db      181 LQAQKYSQDELFKHKNVKIIWDSIRNI-VGENEIEKIVVENVKTKOKTELKADGVFVYI 239

QY      240 GMKPLTAPPKDLGITNDVGVIYTKDDMTTSVPGIFAAGDYRDKGLRQIVTATGDSIAAQ 299
Db      240 GYEPKTELFKDSININKWGIETDENMETNIKGVFAAGDYRSKLIIRQLTTAVSDGTVAAAL 299

QY      300 SAAEYI 305
Db      300 MAEKYI 305
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Search completed: September 15, 2004, 12:21:32
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:05:08 ; Search time 23 Seconds
(without alignments)
724.454 Million cell updates/sec

Title: US-09-825-212-1
Perfect score: 1662
Sequence: 1 MGTEIDFDIAIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1582	95.2	311	1	TRXB_STAAM
2	1455	87.5	310	1	TRXB_STAEP
3	1154	69.4	315	1	TRXB_BACSU
4	1057	63.6	319	1	TRXB_LISIN
5	1054	63.4	319	1	TRXB_LISMO
6	726	43.7	315	1	TRXB_EUBAC
7	706	42.5	315	1	TRXB_GLOLI
8	697.5	42.0	307	1	TRXB_TREPA
9	668	42.0	308	1	R34K_CLOPA
10	644.5	38.8	321	1	TRXB_STRCL
11	641.5	38.6	310	1	TRXB_RICCN
12	639.5	38.5	335	1	TRXB_MYCTU
13	632.5	38.1	458	1	TRXB_MYCLE
14	625.5	37.6	321	1	TRXB_STRCO
15	619.5	37.3	310	1	TRXB_RICPR
16	619.5	37.3	311	1	TRXB_MYCSM
17	605	36.4	312	1	TRXB_CHLTR
18	601	36.2	318	1	TRXB_HAEIN
19	598.5	36.0	333	1	TRBL_ARATH
20	595	35.8	311	1	TRXB_CHLPN
21	593	35.7	312	1	TRXB_CHLMU
22	581.5	35.0	383	1	TRB2_ARATH
23	564.5	34.0	320	1	TRXB_COXBU
24	564.5	34.0	320	1	TRXB_ECOLI
25	564	33.9	307	1	TRXB_MYCRU
26	558	33.6	311	1	TRXB_HELPJ
27	558	33.6	318	1	TRXB_VIBCH
28	554	33.3	311	1	TRXB_HELPY
29	552	33.2	319	1	TRXB_BUCAP
30	551.5	33.2	318	1	TRBL_YEAST
31	550.5	33.1	315	1	TRXB_MYCGE
32	545.5	32.8	309	1	TRXB_UREPA
33	544.5	32.8	334	1	TRXB_NEUCR

RESULT 1

ID	TRXB_STAAM	STANDARD;	PRT;	311 AA.
AC	Q99VL2;			
DT	15-MAR-2004 (Rel. 43, Created)			
DT	15-MAR-2004 (Rel. 43, Last sequence update)			
DE	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Thioredoxin reductase (EC 1.8.1.9) (TRXR).			
GN	TRXB OR SAV0764 OR SA0719 OR MW0726.			
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699),			
OS	Staphylococcus aureus (strain N315), and			
OS	Staphylococcus aureus (strain MW2),			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=158878, 158879, 196620;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Mu50 / ATCC 700699, and N315;			
RC	MEDLINE=21311952; PubMed=11418146;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,			
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,			
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,			
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,			
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,			
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus			
RT	aureus.";			
RL	Lancet 357:1225-1240 (2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Mu50.			
RC	MEDLINE=22040717; PubMed=12044378;			
RA	Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,			
RA	Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,			
RA	Yamamoto K., Hiramatsu K.;			
RT	"Genome and virulence determinants of high virulence community-			
RT	acquired MRSA.";			
RL	Lancet 359:1819-1827 (2002).			
CC	-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide			
CC	+ NADPH.			
CC	-!- COFACTOR: Binds 1 FAD per subunit (By similarity).			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.			
CC	-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide			
CC	oxidoreductase family.			

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EMBL; AP003360; BAB56926.1; -.

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DR EMBL; AP003131; BAB41952.1; -.
DR EMBL; AP004824; BAB94591.1; -.
DR PIR; E89849; E89849.
DR HSP; Q39243; 1VDC.
DR SWISS-2DPAGE; Q99VL2; STAA.
DR InterPro; IPR000759; Adnrdx_reductase.
DR InterPro; IPR001327; FAD_Pyr_redox.
DR InterPro; IPR00103; Pyridine_redox_2.
DR InterPro; IPR008255; Pyr_redox2_AS.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRFS; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome. 42 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 35 137 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 134 137 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 277 286 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;

Query Match 95.2%; Score 1582; DB 1; Length 311;
Best Local Similarity 99.4%; Pred. No. 3.1e-107; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 2;

QY 3 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEVENPFGFEMITGP 62
Db 2 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEVENPFGFEMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKGVP 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKGVP 121
QY 123 GEQELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 182
Db 122 GEQELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 181
QY 183 QRILQDRAFNKDKIDFIWSHTTKSINKEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
Db 182 QRILQDRAFNKDKIDFIWSHTTKSINKEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDKGLRQIVTATGDSIAAQA 302
Db 242 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDKGLRQIVTATGDSIAAQA 301
QY 303 EYIEHLNDQ 312
Db 302 EYIEHLNDQ 311

RESULT 2
TRXB_STREP
ID TRXB STREP STANDARD; PRT; 310 AA.
AC Q8CFY8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR SE0547.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
FT "Genome-based analysis of virulence genes in a non-biofilm-forming
FT Staphylococcus epidermidis strain (ATCC 12228).";

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MoI. Microbiol. 49:1577-1593(2003).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
+ NADPH.
-!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
oxidoreductase family.
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or send an email to license@isb-sib.ch).
-----
CC EMBL; AE016745; AA004144.1; -.
DR InterPro; IPR000759; Adnrdx_reductase.
DR InterPro; IPR001327; FAD_Pyr_redox.
DR InterPro; IPR00103; Pyridine_redox_2.
DR InterPro; IPR008255; Pyr_redox2_AS.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRFS; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome. 42 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 35 137 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 134 137 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 277 286 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 310 AA; 33544 MW; D5D6853667137D88 CRC64;

Query Match 87.5%; Score 1455; DB 1; Length 310;
Best Local Similarity 90.3%; Pred. No. 4.6e-98;
Matches 278; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 3 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEVENPFGFEMITGP 62
Db 2 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEVENPFGFEMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKGVP 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKGVP 121
QY 123 GEQELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 182
Db 122 GEQELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 181
QY 183 QRILQDRAFNKDKIDFIWSHTTKSINKEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
Db 182 QRILQDRAFNKDKIDFIWSHTTKSINKEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDKGLRQIVTATGDSIAAQA 302
Db 242 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDKGLRQIVTATGDSIAAQA 301
QY 303 EYIEHLND 310
Db 302 DYITELKD 309

RESULT 3
TRXB_BACSU
ID TRXB BACSU STANDARD; PRT; 315 AA.
AC P80880; O06971;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```

DE Thioredoxin reductase (EC 1.8.1.9) (TRXR) (General stress protein 35)
DE (GSP35).
GN TRXB OR BSUJ4790.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Denizot F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devane K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Goffeau A., Goltightly E.J., Grandi G.,
RA Ghm S.Y., Glaser P., Goffeau A., Goltightly E.J., Foulger D.,
RA Giuseppe G., Guy B.J., Hgga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holmappel S., Honono S., Hullio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medevic C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumshten E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
RL [3]
RP SEQUENCE OF 1-23.
RC STRAIN=168 / IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463(1997).
CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By heat shock, salt stress, oxidative stress, glucose
CC limitation and oxygen limitation.
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond
CC (By similarity).
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC -----
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RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Kurapkat G.,
RA Jones L.-M., Kaerst U., Knef J., Kuhn M., Kunst F., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Purcell R.,
RA Nordisiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL596173; CAC97848.1; -
CC PUR; AH1759; AH1759.
CC ListList; LIN02621.
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR001327; FAD_Pyr_redox.
CC InterPro; IPR001100; Pyr_redox.
CC InterPro; IPR008255; Pyr_redox2_AS.
CC InterPro; IPR000103; Pyridine_redox_2.
CC InterPro; IPR005982; Thioredox_reduct.
CC Pfam; PF00070; Pyr_redox; 1.
CC PRINTS; PR00419; ADXRTASE.
CC PRINTS; PR00368; FADPNR.
CC PRINTS; PR00411; PNRDRTASE1.
CC PRINTS; PR00469; PNRDRTASEII.
CC TIGRFAMs; TIGR01292; TRX_redox; 1.
CC PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
CC Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome.
FT NP BIND 37 44 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 136 139 REDOX-ACTIVE (BY SIMILARITY).
FT NP BIND 279 288 FAD (FLAVIN PART) (BY SIMILARITY).
FT SEQUENCE 319 AA; 34244 MW; C77D54A952526CC1 CRC64;
SQ
Query Match 63.6%; Score 1057; DB 1; Length 319;
Best Local Similarity 65.8%; Pred. No. 2.6e-69;
Matches 200; Conservative 44; Mismatches 60; Indels 0; Gaps 0;
QY 7 FDIATIGAGPAGTAAVYASRANLKTVMTERGIPGQOMANTEVENFPGFEMITGPDLSL 66
DB 8 YDVIILGAGPAGTAAALYTSRADLDTLMERGVFGQWNTAEVNYPGFDSILGPDLSL 67
QY 67 KMFHAKFGAVYQYQDIKSVEDKGKYKVINFGNKELTAKAVIATGABYKLGVPGEQF 126
DB 68 KMLSGAKQFGAEYAGDIKEVIDGKEFTVTAGSKTYKARAIITATGAHRKLGAGESE 127
QY 127 LGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRAQRI 186
DB 128 LSGRGVSYCAVCDGAFKFKRLVVGGSVAEEGYLTRYADKVTIVHRRDKLRAQRI 187
QY 187 QDRAFKNDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246

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Db 188 QDRAFKDEKVDPIWNTVEIIGDGKKVTVKLSTVDSBSIMPVDGVFIYVGLVPLTK 247
QY 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVDRKGLRQIVTATGDSIAAQAAYIE 306
Db 248 AFLSLGIDEGYIVTDEMTNLPGIFAAAGDVRAKSLRQIVTATGDSGLAGQAQKYVE 307
QY 307 HLND 310
Db 308 ELKE 311
RESULT 5
TRXB LISMO STANDARD; PRT; 319 AA.
AC O32823;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR LMO2478.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
CX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD / Serovar 1/2a;
RA Borovok I., Mislovati M., Cohen G., Aharonowitz Y.;
RT "Isolation, cloning and characterization of the Listeria monocytogenes
RT thioredoxin reductase gene, trxB.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Kurapkat G.,
RA Jones L.-M., Kaerst U., Knef J., Kuhn M., Kunst F., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Purcell R.,
RA Nordisiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC
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CC
CC EMBL; AF009622; AAB63804.1; -
CC EMBL; AL591983; CAD00556.1; -
CC PUR; AF1384; AF1384.
CC FSSP; Q39243; LVDC.
CC ListList; LMO02478; -
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR001327; FAD_Pyr_redox.
CC InterPro; IPR001100; Pyr_redox.
CC InterPro; IPR008255; Pyr_redox2_AS.

```


126 ELGGGVSVYCAVCGGAFFKFKRLFVIGGDSAVEGGTFTTTPADKVTIVHRRDELRAORI 185
 125 ELTGKGVSVYCATCADFFDMEVFVIGGDTAVEEAMFLTKFARKVTIVHRRDELRAAKS 184
 186 IQDRAFKNDKIDFWSHHTTKSINEXDKGVSVTLTSTKDG-----SSETHEADGVFIYI 239
 185 IQEKAFFKNEKLNFMWNTVIEEI-KGDGIVESAVFKNRRTGETVFVPAEEDDTGFIYFI 243
 240 GKKPLTAPPKDLGITNDVGYIVTKDMTTSVPGIFAAAGDVDRDKGLRQIVTATGDSIAAO 299
 244 GYDPSALVEGKLELDETYGIFPDNDNMKNVGVFAAGDIRVKSLRQVVTATADGAIAAV 303
 300 SAAEYIEHL 308
 304 QAEKYEEL 312

RESULT 8
 ID TRXB TREPA STANDARD; PRT; 307 AA.
 AC 083730;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Thioedoxin reductase (EC 1.8.1.9) (TRXR).
 GN TRXB OR TP0814.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Nichols;
 RX MEDLINE=98327770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete.";
 RL Science 281:375-388 (1998).
 CC -1- CATALYTIC ACTIVITY: Thioedoxin + NADP(+) = thioedoxin disulfide
 + NADPH.
 CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond.
 CC -1- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
 oxidoreductase family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE001252; AAC65780.1; -;
 CC PIR; C71278; C71278.
 CC HSP; Q39243; 1VDC.
 CC TIGR; TP0814; -;
 CC InterPro; IPR000759; Adrndx reductase.
 CC InterPro; IPR001327; FAD_pyr_redox.
 CC InterPro; IPR001100; Pyr_redox.
 CC InterPro; IPR008255; Pyr_redox2 AS.
 CC InterPro; IPR00103; Pyridine_redox_2.
 CC InterPro; IPR005982; Thioedox_reduct.
 CC Pfam; PF00070; pyr_redox; 1.
 CC PRINTS; PR00419; ADXRDTASE.
 CC PRINTS; PR00368; FADPNR.

126 ELGGGVSVYCAVCGGAFFKFKRLFVIGGDSAVEGGTFTTTPADKVTIVHRRDELRAORI 185
 125 ELTGKGVSVYCATCADFFDMEVFVIGGDTAVEEAMFLTKFARKVTIVHRRDELRAAKS 184
 186 IQDRAFKNDKIDFWSHHTTKSINEXDKGVSVTLTSTKDG-----SSETHEADGVFIYI 239
 185 IQEKAFFKNEKLNFMWNTVIEEI-KGDGIVESAVFKNRRTGETVFVPAEEDDTGFIYFI 243
 240 GKKPLTAPPKDLGITNDVGYIVTKDMTTSVPGIFAAAGDVDRDKGLRQIVTATGDSIAAO 299
 244 GYDPSALVEGKLELDETYGIFPDNDNMKNVGVFAAGDIRVKSLRQVVTATADGAIAAV 303
 300 SAAEYIEHL 308
 304 QAEKYEEL 312

RESULT 7
 ID TRXB CLOLI STANDARD; PRT; 315 AA.
 AC P52213;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Thioedoxin reductase (EC 1.8.1.9) (TRXR).
 GN TRXB.
 OS Clostridium litoreale (Bacterium W6).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1557;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=96096738; PubMed=8529640;
 RA Kreimer S., Andreesen J.R.;
 RT "Glycine reductase of Clostridium litoreale. Cloning, sequencing, and
 molecular analysis of the grdAB operon that contains two in-frame TGA
 codons for selenium incorporation.";
 RL Eur. J. Biochem. 234:192-199 (1995).
 CC -1- CATALYTIC ACTIVITY: Thioedoxin + NADP(+) = thioedoxin disulfide
 + NADPH.
 CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond.
 CC -1- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
 oxidoreductase family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U24268; AAC43575.1; -;
 CC PIR; S63990; S63990.
 CC HSP; Q39243; 1VDC.
 CC InterPro; IPR000759; Adrndx reductase.
 CC InterPro; IPR001327; FAD_pyr_redox.
 CC InterPro; IPR001100; Pyr_redox.
 CC InterPro; IPR008255; Pyr_redox2 AS.
 CC InterPro; IPR00103; Pyridine_redox_2.
 CC InterPro; IPR005982; Thioedox_reduct.
 CC Pfam; PF00070; pyr_redox; 1.
 CC PRINTS; PR00419; ADXRDTASE.
 CC PRINTS; PR00368; FADPNR.
 CC PRINTS; PR00411; PNDRDTASEI.
 CC PRINTS; PR00469; PNDRDTASEII.
 CC TIGRfam; TIGR01292; TRX_reduct; 1.
 CC PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
 FT NP BIND 34 41 FAD (ADP PART) (BY SIMILARITY).
 FT DISULFID 134 137 REDOX-ACTIVE (BY SIMILARITY).
 FT NP BIND 282 291 FAD (FLAVIN PART) (BY SIMILARITY).
 SQ SEQUENCE 315 AA; 33946 MW; 2CA55D36E579B2EF CRC64;
 Query Match 42.5%; Score 706; DB 1; Length 315;
 Best Local Similarity 48.5%; Pred. No. 5.6e-44;
 Matches 150; Conservative 53; Mismatches 98; Indels 8; Gaps 3;
 QY 7 FDIATIGAGPAGTAAVYASRANLKTVMIERGIPGGQMANTTEVENFPG-FEMITGPDLS 65
 DB 5 YDIATIGSGPAGLAALYGARAKCKTLLLEGMKVGQIVITHEVANYPGSVPEATGSLI 64
 QY 66 TKMFEHAKFKGAVYQYQYCDIKSVDRDKGEYKVINFGNKKELTAKAVIITATGAEYKKIGVPGSQ 125
 DB 65 GRMEEQVEFGAERVDNIVDFDTDKIKVLKGAKEGYKAKAVIVATGASPKLAGCPGK 124

[illegible]

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RT Streptomyces clavuligerus and its possible role in beta-lactam
RT antibiotic biosynthesis."
RL J. Bacteriol. 175:623-629(1993).
CC -!- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system which may be involved in biosynthesis of penicillins and
CC cephalosporins and may be important in determining the thiol-
CC disulfide redox balance.
CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC -----
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CC -----
EMBL; Z21946; CAA79940.1; -.
DR HSP; A53307; A53307.
DR HSP; P09625; ICL0.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001327; FAD_Pyr_redux.
DR InterPro; IPR001100; Pyr_redux.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR InterPro; IPR000103; Pyridine_redux_2.
DR InterPro; IPR005982; Thioredux_reduct.
DR Pfam; PF00070; Pyr_redux; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNRDRTASEI.
DR PRINTS; PR00469; PNRDRTASEII.
DR TIGRFAMs; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
KW INIT MET 0
FT NP_BIND 33 41 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 135 138 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND 278 287 FAD (FLAVIN PART) (BY SIMILARITY).
FT SEQUENCE 321 AA; 34015 MW; 4C2B01AADC5A0FDF CRC64;

Query Match 38.8%; Score 644.5; DB 1; Length 321;
Best Local Similarity 45.6%; Pred. No. 1.6e-39;
Matches 140; Conservative 53; Mismatches 109; Indels 5; Gaps 5;

QY 8 DIAIIGAGPAGMTAAVYASRANLKTVMTERGI-PGGQMANTTEVENFPFGP-EMITGPDLS 65
DB 5 NVIIIGSPAGYTAALYTARASLQPLVFEAGVATGAGLMTTIDVENFPFGDINGMPDLM 64
QY 66 TKMPFHAKKFGAVYQYGDIKSVEDGEYK-VINFGNKELTAKAVIIATGAEEKYGVGPE 124
DB 65 DNMRAQAEFAGLPPDDVVSVDLTGDKITVDSAGTVHRAKAVITVTSQARKLGLPRE 124
QY 125 QELGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRAQR 184
DB 125 DALSRGVSWCATCDGFFPKQDQIVVVGSDGTAMEEATFLSRFAKSVTVIHRDLSIRASK 184
QY 185 ILQDRAFNKDKIDFTWSHTTKSINEXKGVGVTVTTSKDGSEETHADGVFIYGMKPL 244
DB 185 AMQDRAFAADPKISFAWNSEVATIHGEQ-KLTGLTLRDTKTGETRELATGLFIAVGHDP 243
QY 245 TAPFDKDLGINTDVGVI-VTKDDMTTSVPGIPEAGDVDRKGLQIVTATGDSGIAAQSAE 303
DB 244 TELFKQLDDBEGYLLKVASPSTRNLTGVFAAGOVVDHTYQAIATAGTGCSAALDAER 303
QY 304 YIEHLND 310
DB 304 YLAALAD 310

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RESULT 11

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TXRB_RICCN STANDARD; PRT; 310 AA.
ID TRXB_RICCN
AC Q92I02;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR RC0618.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsia;
OC NCBI_TaxID=781;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RA "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
RL -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC -----
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CC -----
EMBL; AE008622; AAL03156.1; -.
DR PIR; B97777; B97777.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001327; FAD_Pyr_redux.
DR InterPro; IPR001100; Pyr_redux.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR InterPro; IPR000103; Pyridine_redux_2.
DR InterPro; IPR005982; Thioredux_reduct.
DR Pfam; PF00070; Pyr_redux; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNRDRTASEI.
DR PRINTS; PR00469; PNRDRTASEII.
DR TIGRFAMs; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
KW Complete proteome.
FT NP_BIND 34 41 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 135 138 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND 281 290 FAD (FLAVIN PART) (BY SIMILARITY).
FT SEQUENCE 310 AA; 33469 MW; 0F1E04D6BC7E111B CRC64;

Query Match 38.6%; Score 641.5; DB 1; Length 310;
Best Local Similarity 46.0%; Pred. No. 2.5e-39;
Matches 144; Conservative 45; Mismatches 107; Indels 17; Gaps 6;

QY 4 EIDFDIATIGAGPAGMTAAVYASRANLKTVMTERGI-PGGQMANTTEVENFPFGP-EMITGP 62
DB 2 KITTKVLIIGSGFAGLSAALYTARAAALFKPILNGMQPGQLTITTDVENYPPGFAETVQGP 61
QY 63 DLSTQMFHAKKFGAVYQYGDIKSVY-DKGEYVINFNGNKELTAKAVIIATGAEEKYKIGV 121

```


DR InterPro; IPR005746; Thioredoxin.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR Pfam; PF00085; thioRed; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thioredoxin; 1.
 DR TIGRfam; TIGR01292; TRX_reduct; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
 DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
 KW Electron transport; Complete proteome.
 FT DOMAIN 1 321
 FT THIOREDOXIN REDUCTASE.
 FT DOMAIN 322 347
 FT THIOREDOXIN.
 FT NP BIND 41 48
 FT FAD (ADP PART) (BY SIMILARITY).
 FT DISULFID 142 145
 FT REDOX-ACTIVE (BY SIMILARITY).
 FT NP BIND 285 294
 FT FAD (FLAVIN PART) (BY SIMILARITY).
 FT DISULFID 379 382
 FT REDOX-ACTIVE (BY SIMILARITY).
 SQ SEQUENCE 458 AA; 49046 MW; 84D367AB31899987 CRC64;
 Query Match 38.1%; Score 632.5; DB 1; Length 458;
 Best Local Similarity 45.3%; Pred. No. 1.8e-38;
 Matches 140; Conservative 53; Mismatches 111; Indels 5; Gaps 5;
 QY 8 DIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTVEENPFPGFEM-ITGPDLSLT 66
 DB 13 EVIVGSGPAGYTAALYAAQAQLTPLVFEGTSFGGALMTTEVENYFGFRNGITGPELMD 72
 QY 67 KMEFAHAKFGAVYQYGDIKSVEDKGEYK-VINFGNKELTAKAVIATGAAYKKIGVPEQ 125
 DB 73 DMREQLRFGAELRTEDVESLSLRGPIKSVTVTAEGQYQARAVILAMGTSVRYLIQIFGEQ 132
 QY 126 ELGRGVSYCAVCDGAFKKRRLFVIGGGSAAVEGFTTKFADKVTIVHRRDELRAQRI 185
 DB 133 ELLGRGVSAATCDGSPFRGQDIAVIGGGSAAVEEALFLTRFARSVTLVHRRDEFRASKI 192
 QY 186 LQPAFKNKIDFTWSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLT 245
 DB 193 MLGRARNNDKIKFITNHTVAVNGYTTVTG-LRLNNTTGTETTLVTVGVFVAIGHPEPS 251
 QY 246 APFRDLGITNDVGVYIVTKDDMT-TSVFGIFAAAGVRDKGLRQIVTATDGDGSIQAQAAEY 304
 DB 252 SLVSDVDVIDPDGYVLVKGRTTSTMDGVFAAGDLVDRTYRQAITAAGSGCAAIDAERW 311
 QY 305 I-EHLNDOA 312
 DB 312 LAEHAGSKA 320
 RESULT 14
 TRXB_STRCO STANDARD; PRT; 321 AA.
 AC P52215;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
 GN TRXB OR SCO3890 OR SCH24.12C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA MEDLINE=99014240; PubMed=9795152;
 RX Gal-Mor O., Borovok I., Av-Gay Y., Cohen G., Aharonowitz Y.;
 RT "Gene organization in the trxA/B-oriC region of the Streptomyces
 RL coelicolor chromosome and comparison with other eubacteria.";
 RL Gene 217:83-90(1998).

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bifunctional thioredoxin reductase/thioredoxin [Includes: Thioredoxin
 DE reductase (EC 1.8.1.9) (TRXR); Thioredoxin].
 GN TRXB/A OR TRX OR ML2703.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97124199; PubMed=8969512;
 RA Feihl H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G.,
 RT Takiff H.E., Eiglmeyer K., Bergh S., Cole S.T.;
 RT "Gene arrangement and organization in an approximately 76 kb fragment
 RT encompassing the oric region of the chromosome of Mycobacterium
 RL leprae.";
 RL Microbiol. 142:3147-3161(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96059638; PubMed=7476189;
 RA Wieleb B., van Soelingen D., Holmgren A., Offringa R., Ottenhoff T.,
 RA Thole J.;
 RT "Unique gene organization of thioredoxin and thioredoxin reductase in
 RT Mycobacterium leprae.";
 RL Mol. Microbiol. 16:921-929(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
 CC + NADPH.
 CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
 CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
 CC oxidoreductase family.
 CC -!- SIMILARITY: Belongs to the thioredoxin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L39923; AAB53131.1; -;
 DR EMBL; X87899; CA61150.1; -;
 DR EMBL; AL583926; CAC32235.1; -;
 DR FIR; S77662; S77662.
 DR HSP; P80579; 1QWU.
 DR Leproma; ML2703; -;
 DR InterPro; IPR000759; Adrndx_reductase.
 DR InterPro; IPR001327; FAD_Pyr_redox.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR008255; Pyr_redox2_AS.
 DR InterPro; IPR00103; Pyridine_redox_2.
 DR InterPro; IPR006662; Thiored.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR InterPro; IPR005982; Thioredox_reduct.

Query Match	37.6%;	Score 625.5;	DB 1;	Length 321;
Best Local Similarity	43.7%;	Pred. NO. 3.8e-38;		
Matches 136;	Conservative 56;	Mismatches 114;	Indels 5;	Gaps 5;

QY	8	DIALIAGPAGMTAAVVASRANLKVTVMIERGI-PGGQWANTERVENPFPGF-EMITGPDLS	65
DB	5	NVIILGGSPAGYTAALYATASRLKPLVPEGAVTAGGALMNTTEVENFFQDQIMGPELM	64
QY	66	TKMFEHAKKFGAVYQYGDIDKSVEDKGEYK-VINFGNKELTAKAVIIATGAEYKIGVPGE	124
DB	65	DNMRAQAEFGEALLPDDVVAVDLSGBIKVTTDTAGTVHRAKAVIVITGSGHRKLGLE	124
QY	125	QELGGRGVSYCAVCGDAGFFRNKRLFLVIGGGDSVAVEGTFTTKPADKVTIVHRRDELRAQR	184
DB	125	DALSGRGVSWCATCDGFFKQDQIDVAVIGGGDTAMEEATFLSRFAKSVTVIHRDRTLRSK	184
QY	185	ILODRAFNDKIDFIWSHHTKSINEKDGKVGSVTLTSTKDGSEBTHEADGVFIYIGMKPL	244
DB	185	AMQERAFADPKISFVMDSEVAEV-QGQKLAGLKLNRVKTGELSPLVPTGLFIAIGHDPR	243
QY	245	TAPFKDLGINDVGYI-VTKDDMTTSVPGIPFACGDYRDKGLRQIVATRGDSGTAAQSAE	303
DB	244	TELFKQGLDLPQGYLKVADPSTRTNLTVFGAGDVVDHTYRQAITAAGTCSAAVDAEP	303
QY	304	YIEHLNDQARS 314	
DB	304	FLAALSDEKA 314	

RESULT 15				
TRXB_RICPR				
ID	TRXB_RICPR	STANDARD;	PRT;	310 AA.
AC	Q9ZD37;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Thioredoxin reductase (EC 1.8.1.9) (TRXR).			
GN	TRXB OR RP445.			
OS	Rickettsia prowazekii.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			
OC	Rickettsiaceae; Rickettsiae; Rickettsia.			
OX	NCBI_TaxID=782;			
XP	[1]			
RP	SEQUENCE FROM N.A.			
RN	STRAIN=Madrid E;			
RC	MEDLINE=99039499; PubMed=9823893;			
RA	Andersson S.G.E., Zomorodipour A., Andersson J.O.,			
RA	Sicheritz-Ponten T., Almark U.C.M., Podowski R.M., Naeslund A.K.,			
RA	Eriksson A.-S., Winkler H.H., Kurland C.G.;			
RT	"The genome sequence of Rickettsia prowazekii and the origin of			
RT	mitochondria."			
RL	Nature 396:133-140(1998).			
CC	!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide			
CC	+ NADPH.			
CC	!- COFACTOR: Binds 1 FAD per subunit (By similarity).			
CC	!- SUBUNIT: Homodimer (By similarity).			
CC	!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	!- MISCELLANEOUS: The active site is a redox-active disulfide bond.			
CC	!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide			
CC	oxido-reductase family.			

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entities requires a license agreement (See http://www.isb-sib.ch/announce/	
or send an email to license@isb-sib.ch).	

EMBL; AJ235271; CAAL4902.1; -	
PIR; D71703; D71703.	
HSSP; P09625; 1TRB.	
InterPro; IPR000759; Adrndx reductase.	

Wed Sep 15 13:38:57 2004

us-09-825-212-1.rsp

```

DR InterPro; IPR001327; FAD pyr_redox.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR008255; Pyr_redox2 AS.
DR InterPro; IPR000103; Pyridine_redox 2.
DR InterPro; IPR005982; ThioRedox_redox.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; ENDRDTASEI.
DR PRINTS; PR00469; ENDRDTASEII.
DR TIGRFAMs; TIGR01292; TRX_redox; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX 2; 1.
KW Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome.
FT NP_BIND 34 41 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 135 138 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND 281 290 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 310 AA; 33582 MW; 573CA975C750957D CRC64;

Query Match 37.3%; Score 619.5; DB 1; Length 310;
Best Local Similarity 45.2%; Pred. No. 9.8e-38;
Matches 140; Conservative 48; Mismatches 111; Indels 11; Gaps 5;

QY 4 EIDFDIAIIGAGPAGMTAAVYASRANIKTVMIERGIPIGGOMANTEVEENPPGF-EMITGP 62
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 2 KITTKVLIIGSGPAGLSAAIYTARSALKPILINGMQPGQLTMTDVENYPGFAETIQGP 61
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 DLSTKMFHAKKFGAVQYGDIKSVE-DKGEYKVINFNGKELTAKAVIIATGAEYKKIGV 121
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 62 WLMEQMSMQAKNVGTEIISDYVERVDLSKRPFKIFTGTGNEYEADSIICTAESKWLGI 121
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 122 PGQELGGRGVSYCAVCDGAFKKNRFLVIGGDSAVEEGTFTTKPADKVTIVHRRDEL 181
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 122 ASEQFRGFGVSSCAICDGRFFKQEIWVGGSNSALEEALYLTNHANKVTVVHRRNSFR 181
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 182 AQRILQDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLTSTKDGSEETHE-----ADGVF 236
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 182 AEKILQDRLEKPKISVIWDHI---IDIEIVGSNPKPAGTVGKIQNVYINEINLVNCSGVF 238
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 237 IYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-TSVPGIFAAGVDKGLRQIVTATGDGS 295
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 IAIQHAFNTALFKGQIAIDDDNYIVTQSGSTRITNVEGVFAAGVDQDKIYRQAVTAAASGC 298
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 296 IAAQSAAEYI 305
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 299 MALEVAKFL 308
Db : |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

Search completed: September 15, 2004, 12:16:34
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:12:53 ; Search time 115 Seconds
(without alignments)
877.964 Million cell updates/sec

Title: US-09-825-212-1
Perfect score: 1662
Sequence: 1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacterioph.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						Description	
Result No.	Score	Match	Length	DB	ID		
1	1582	95.2	311	2	054079	O54079 staphylococ	
2	1582	95.2	311	16	Q99VL2	Q99VL2 staphylococ	
3	1487	89.5	291	2	Q9X07	Q9X07 staphylococ	
4	1455	87.5	310	16	Q8CP8	Q8CP8 staphylococ	
5	1173	70.6	318	16	Q81X56	Q81X56 bacillus an	
6	1170	70.4	321	16	Q81531	Q81531 bacillus ce	
7	1146	69.0	315	16	Q8CX98	Q8CX98 oceanobacil	
8	1145.5	68.9	315	16	Q8K703	Q8K703 bacillus ha	
9	943	56.7	312	16	Q88Y17	Q88Y17 lactobacill	
10	940	56.6	304	16	Q83N8	Q83N8 enterococcu	
11	899	54.1	305	16	Q8N2Y5	Q8N2Y5 streptococ	
12	897	54.0	305	16	Q8K6D5	Q8K6D5 streptococ	
13	882	53.1	304	16	Q8DVL7	Q8DVL7 streptococ	
14	872	52.5	308	16	Q9CH02	Q9CH02 lactococcu	
15	852.5	51.3	304	16	Q8E773	Q8E773 streptococ	
16	852.5	51.3	304	16	Q8E1Q9	Q8E1Q9 streptococ	

17	851	51.2	303	16	Q8DP78	Q8dp78 streptococ
18	849	51.1	303	16	Q97PY2	Q97py2 streptococ
19	815	49.0	310	2	Q93FC9	Q93fc9 lactobacill
20	753	45.3	314	2	Q9EV96	Q9ev96 clostridium
21	746	44.9	305	16	Q8R817	Q8r817 thermoanaer
22	741	44.6	308	16	Q8R8V8	Q8r8v8 thermoanaer
23	738.5	43.8	325	16	Q9RSY7	Q9rsy7 deinococcus
24	687	41.3	317	16	Q9WZX3	Q9wzx3 thermotoga
25	682.5	41.1	311	16	Q8KE48	Q8ke48 chlorobium
26	671	40.4	308	16	Q97KP8	Q97kp8 clostridium
27	647.5	39.0	341	16	Q8G6J1	Q8g6j1 bifidobacte
28	645.5	38.8	345	17	Q9VQ08	Q9vq08 pyrococcus
29	643.5	38.7	336	17	Q50134	Q50134 pyrococcus
30	641.5	38.6	336	2	Q93AQ4	Q93aq4 mycobacteri
31	639.5	38.5	356	17	Q8U108	Q8u108 pyrococcus
32	638.5	38.4	305	17	Q8PUI1	Q8puil methanosarc
33	635.5	38.2	335	16	Q7TVC8	Q7tvc8 mycobacteri
34	634	38.1	313	16	Q8FSW1	Q8fsw1 corynebacte
35	629.5	37.9	326	16	Q8RS12	Q8ris2 streptomyc
36	626	37.7	315	16	Q897A0	Q897a0 clostridium
37	625	37.6	317	16	Q8NLS9	Q8nls9 corynebacte
38	622.5	37.5	315	17	Q8TR16	Q8tr16 methanosarc
39	613.5	36.9	323	16	Q82FE8	Q82fe8 streptomyc
40	606	36.5	320	16	Q8EUJ3	Q8euj3 mycoplasma
41	604	36.3	318	2	Q9X5F7	Q9x5f7 zymomonas m
42	599.5	36.1	303	17	Q26804	Q26804 methanobact
43	596.5	35.9	556	16	Q8XMA7	Q8xma7 clostridium
44	594.5	35.8	333	10	Q84W20	Q84w20 arabidopsis
45	592.5	35.6	453	16	Q8DHM2	Q8dhm2 synechococ

ALIGNMENTS

RESULT 1

O54079 PRELIMINARY; PRT; 311 AA.

AC O54079; Q9RL89;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Thioredoxin reductase (EC 1.6.4.5) (Thioredoxine reductase).

GN TRXB

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Oxford;

RA Uziel O., Borovok I., Schreiber R., Aharonowitz Y., Cohen G.;

RT "Transcriptional analysis of the thioredoxin (trxB) and thioredoxin reductase (trxB) genes from Staphylococcus aureus";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Oxford;

RA Borovok I.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-RUSA277;

EX MEDLINE=20031141; PubMed=10566865;

RA de Lencastre H., Wu S.W., Pinho M.G., Ludovice A.M., Filipe S.,

RA Gardete S., Sobral R., Gill S., Chung M., Tomasz A.;

RT "Antibiotic resistance as a stress response: complete sequencing of a large number of chromosomal loci in Staphylococcus aureus strain COL that impact on the expression of resistance to methicillin."

RL Microb. Drug Resist. 5:163-175(1999).

DR EMBL; AJ223781; CAAL1546.2; -

DR EMBL; Y18636; CAB60740.1; -

DR PIR; B9849; E89849.

DR HSSP; Q39243; 1VDC.

GO; GO:0005737; C:cytoplasm; IEA.

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RL aureus". Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA".
 RL Lancet 359:1819-1827(2002).
 CC !- COFACTOR: FAD (BY SIMILARITY).
 DR EMBL; AF003360; BAB56926.1; -;
 DR EMBL; AF003131; BAB41952.1; -;
 DR EMBL; AF004824; BAB94591.1; -;
 DR PIR; E89849; E89849.
 DR HSSP; Q39243; 1VDC.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrnx reductase.
 DR InterPro; IPR001327; FAD pyr reduct.
 DR InterPro; IPR000103; Pyridine reduct_2.
 DR InterPro; IPR001100; Pyr reduct.
 DR InterPro; IPR008255; Pyr reduct_2 AS.
 DR InterPro; IPR005982; Thioredox_reduct.
 DR Pfam; PF00070; Pyr reduct; 1.
 DR PRINTS; PR00419; ADXRTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRFAMS; TIGR01292; TRX reduct; 1.
 DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
 DR FAD; Flavoprotein; Oxidoreductase; Complete proteome.
 KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;

Query Match 95.2%; Score 1582; DB 16; Length 311;
 Best Local Similarity 99.4%; Pred. No. 2e-104;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENFPFGFEMITGP 62
 Db 2 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENFPFGFEMITGP 61
 Qy 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAQAVIIATGAETKGIQVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAQAVIIATGAETKGIQVP 121
 Qy 123 GEQELGGRGVSVCVCGAFKFKRLFVIGGDSAVEEGTFTKFAKVTIVHRRDELRA 182
 Db 122 GEQELGGRGVSVCVCGAFKFKRLFVIGGDSAVEEGTFTKFAKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFNKDKIDFWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFNKDKIDFWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVDRKGLRQIVTATGDSIAAQSAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVDRKGLRQIVTATGDSIAAQSAA 301
 Qy 303 EYIEHLNDQA 312
 Db 302 EYIEHLNDQA 311
 RESULT 3
 Q9KX07
 ID Q9KX07 PRELIMINARY; PRT; 291 AA.

DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrnx reductase.
 DR InterPro; IPR001327; FAD pyr reduct.
 DR InterPro; IPR000103; Pyridine reduct_2.
 DR InterPro; IPR001100; Pyr reduct.
 DR InterPro; IPR008255; Pyr reduct_2 AS.
 DR InterPro; IPR005982; Thioredox_reduct.
 DR Pfam; PF00070; Pyr reduct; 1.
 DR PRINTS; PR00419; ADXRTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRFAMS; TIGR01292; TRX reduct; 1.
 DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
 DR Oxidoreductase.
 KW Oxidoreductase.
 SQ SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;

Query Match 95.2%; Score 1582; DB 2; Length 311;
 Best Local Similarity 99.4%; Pred. No. 2e-104;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENFPFGFEMITGP 62
 Db 2 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEENFPFGFEMITGP 61
 Qy 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAQAVIIATGAETKGIQVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAQAVIIATGAETKGIQVP 121
 Qy 123 GEQELGGRGVSVCVCGAFKFKRLFVIGGDSAVEEGTFTKFAKVTIVHRRDELRA 182
 Db 122 GEQELGGRGVSVCVCGAFKFKRLFVIGGDSAVEEGTFTKFAKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFNKDKIDFWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFNKDKIDFWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVDRKGLRQIVTATGDSIAAQSAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVDRKGLRQIVTATGDSIAAQSAA 301
 Qy 303 EYIEHLNDQA 312
 Db 302 EYIEHLNDQA 311
 RESULT 2
 Q99VL2
 ID Q99VL2 PRELIMINARY; PRT; 311 AA.
 AC Q99VL2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thioredoxine reductase.
 GN TRXB OR SAV0764 OR SA07119 OR WM0726.
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699), and
 OS *Staphylococcus aureus* (strain N315), and
 OS *Staphylococcus aureus* (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=158878, 158879, 196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

AC 09X07;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL;
 RX MEDLINE=20031141; PubMed=10566865;
 RA de Lencastre H., Wu S.W., Pinho M.G., Ludovice A.M., Filipe S.,
 RA Gardner S., Sobral R., Gill S., Chung M., Tomasz A.;
 RT "Antibiotic resistance as a stress response: complete sequencing of a
 RT large number of chromosomal loci in Staphylococcus aureus strain COL
 RT that impact on the expression of resistance to methicillin.";
 RL Microb. Drug Resist. 5:163-175(1999).
 DR EMBL; Y14324; CAB82468.1; -;
 DR HSP; Q39243; 1VDC.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR001327; FAD_pyr_redux.
 DR InterPro; IPR00103; Pyridine_redux_2.
 DR InterPro; IPR008255; Pyr_redux.
 DR InterPro; IPR005982; Thio_redux_reduct.
 DR Pfam; PF00070; Pyr_redux; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR TIGRFAMS; TIGR01292; TRX_reduct; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 291 AA; 31640 MW; 3C700EE8752343CF CRC64;
 Query Match 89.5%; Score 1487; DB 2; Length 291;
 Best Local Similarity 99.3%; Pred. No. 1e-97;
 Matches 289; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 22 AVASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLS TKMFHAKKFGAVYQY 81
 Db 1 AVASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLS TKMFHAKKFGAVYQY 60
 QY 82 GIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVPGQEQLGGRGVSVCVCDGA 141
 Db 61 GIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVPGQEQLGGRGVSVCVCDGA 120
 QY 142 FFKNKL FVIGGDSAVERTTKEADKVTIVHRRDELRAQRILODRAPKNDKIDFIWS 201
 Db 121 FFKNKL FVIGGDSAVERTTKEADKVTIVHRRDELRAQRILODRAPKNDKIDFIWS 180
 QY 202 HTTKS INEKDGKVS VTLTSTKDGSETHADGVFIYIGMKPLTAPFKDLGINTDVGIV 261
 Db 181 HTLKS INEKDGKVS VTLTSTKDGSETHADGVFIYIGMKPLTAPFKDLGINTDVGIV 240
 QY 262 TKDDMTTSVPGIFAGDVRDKGLRQIVTATDGSIAAQAAYIEHLNDQA 312
 Db 241 TKDDMTTSVPGIFAGDVRDKGLRQIVTATDGSIAAQAAYIEHLNDQA 291
 RESULT 4
 Q8CPY8 PRELIMINARY; PRT; 310 AA.
 AC Q8CPY8;
 DT 01-NAR-2003 (Tremblrel. 23, Created)
 DT 01-NAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Thioredoxine reductase.
 GN SE0547.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016745; AAC04144.1; -;
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrndx_reductase.
 DR InterPro; IPR001327; FAD_pyr_redux.
 DR InterPro; IPR00103; Pyridine_redux_2.
 DR InterPro; IPR001100; Pyr_redux.
 DR InterPro; IPR008255; Pyr_redux2_AS.
 DR InterPro; IPR005982; Thio_redux_reduct.
 DR Pfam; PF00070; Pyr_redux; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR TIGRFAMS; TIGR01292; TRX_reduct; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 310 AA; 33544 MW; D5D6853667137D8B CRC64;
 Query Match 87.5%; Score 1455; DB 16; Length 310;
 Best Local Similarity 90.3%; Pred. No. 2.1e-95;
 Matches 278; Conservative 17; Mismatches 13; Indels 0; Gaps 0;
 QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP 62
 Db 2 TEVDFDVAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP 61
 QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVP 121
 QY 123 GEQLGGRGVSVCVCDGAFFKNKRL FVIGGDSAVEEGFTTTPKADKVTIVHRRDELRA 182
 Db 122 GEQLGGRGVSVCVCDGAFFKNKRL FVIGGDSAVEEGFTTTPKADKVTIVHRRDELRA 181
 QY 183 QRILQDRAPKNDKIDFIWSHTTKS INEKDGKVS VTLTSTKDGSETHADGVFIYIGMK 242
 Db 182 QNLIQERAPKNDKIDFIWSHTTKS INEKDGKVS VTLTSTKDGSETHADGVFIYIGMK 241
 QY 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAGDVRDKGLRQIVTATDGSIAAQAAS 302
 Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAGDVRDKGLRQIVTATDGSIAAQAAS 301
 QY 303 EYIEHLND 310
 Db 302 DYITELKD 309
 RESULT 5
 Q8IX56 PRELIMINARY; PRT; 318 AA.
 AC Q8IX56;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Thioredoxin reductase.
 GN TRXB OR BA5387.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;

RESULT 6	Q015J1	RESULT 7
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RESULT 6	Q015J1	RESULT 7
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Q8CX98 Q8CX98 PRELIMINARY; PRT; 315 AA.
 AC Q8CX98;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thioresoxin reductase (NADPH) (General stress protein)
 DE (EC 1.6.4.5).
 GN OB2469.
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments.";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL; AP004601; BAC14425.1; -;
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPRO00759; Adirndx_reductase.
 DR InterPro; IPRO01327; FAD_pyr_redux.
 DR InterPro; IPRO01100; Pyr_redux_2.
 DR InterPro; IPRO08255; Pyr_redux2_AS.
 DR InterPro; IPRO03042; Rng_mnoxygenase.
 DR InterPro; IPRO005982; Thioresoxin_reduct.
 DR Pfam; PF00070; Pyr_redux_1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEII.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRfams; TIGR01292; TRX_reduct; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 315 AA; 34337 MW; 6F0ED957848374F1 CRC64;
 Query Match 69.0%; Score 1146; DB 16; Length 315;
 Best Local Similarity 69.1%; Pred. No. 1.9e-73;
 Matches 217; Conservative 39; Mismatches 58; Indels 0; Gaps 0;
 QY 1 MGTETDIDFALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEVENPFGFEMIT 60
 DB 1 MSEERMYDVIAGAGPAGMTAAVYASRANLDTMLERGIPGGQMANTEVENPFGFNL 60
 QY 61 GDLSTKMFHAKKFGAVYQDVKSVKYNFNGKELTAKAVIATGAEYKKG 120
 DB 61 GDLNKNMFHAKKFGAAAYAGDIKEVEDHGEYKLIKAGSKEYYRSLIATGAQYKKG 120
 QY 121 VPGEELGGRGVSCAVCDGAFKKNRKLPIVIGSDSAVEEGFTTKFADKVTIVHRRDL 180
 DB 121 IEGEALSGRGVSCAVCDGAFKKNRLVVIIGGSDSAVEEGHYLTFRANKVTIVHRRDL 180
 QY 181 RAQRIQDRAFNKDKIDFVWSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIY 240
 DB 181 RAQRIQDRAFNKDKIDFVWSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIY 240
 QY 241 MKPLTAPFDLIGITNDVGVIVTKDDMTTSVPGIIFAAGDVDRKGLRQIVTATGDSIAAQ 300
 DB 241 MVPLNQALSLGIIITNDVGVIVTKDDMTTSVPGIIFAAGDVDRKGLRQIVTATGDSIAAQ 300
 QY 301 AAEYIEHLNDQARS 314
 DB 301 AIKYVEDLEEKIS 314

RESULT 8
 Q9K703 Q9K703 PRELIMINARY; PRT; 315 AA.
 AC Q9K703;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Thioresoxin reductase (NADPH) (EC 1.6.4.5).
 GN TRXB OR BH3571.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- COFACTOR: FAD (BY SIMILARITY).
 DR EMBL; AP001519; BAB07290.1; -;
 DR HSSP; Q39243; 1VDC.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPRO00759; Adirndx_reductase.
 DR InterPro; IPRO01327; FAD_pyr_redux.
 DR InterPro; IPRO01100; Pyr_redux_2.
 DR InterPro; IPRO08255; Pyr_redux2_AS.
 DR InterPro; IPRO03042; Rng_mnoxygenase.
 DR InterPro; IPRO005982; Thioresoxin_reduct.
 DR Pfam; PF00070; Pyr_redux_1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRfams; TIGR01292; TRX_reduct; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 315 AA; 34317 MW; 706FD6CA01D68819 CRC64;
 Query Match 68.9%; Score 1145.5; DB 16; Length 315;
 Best Local Similarity 68.6%; Pred. No. 2e-73;
 Matches 216; Conservative 38; Mismatches 60; Indels 1; Gaps 1;
 QY 1 MGTETDIDFALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEVENPFGFEMI 59
 DB 1 MGEEKYDVVVIAGAGPAGMTAAVYASRANLSTVMVERGVPGQWANTEDVENYFGDHI 60
 QY 60 TGPDLSTKMFHAKKFGAVYQDVKSVKYNFNGKELTAKAVIATGAEYKKG 119
 DB 61 LGPELSTKMFHAKKFGAAAYAGDIKEIDGDLKLVKAGNKEYKARAVIATGAEYKKG 120
 QY 120 GVPGEELGGRGVSCAVCDGAFKKNRKLPIVIGGSDSAVEEGFTTKFADKVTIVHRRDL 179
 DB 121 GVPGEELGGRGVSCAVCDGAFKKNRKLPIVIGGSDSAVEEGHYLTFRANKVTIVHRRDL 180
 QY 180 LRAQRIQDRAFNKDKIDFVWSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIY 239
 DB 181 LRAQRIQDRAFNKDKIDFVWSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIY 240
 QY 240 GMKPLTAPFDLIGITNDVGVIVTKDDMTTSVPGIIFAAGDVDRKGLRQIVTATGDSIAAQ 299
 DB 241 GMLPLNEAVNLTINDEGYIVTNEEMETSVPGIIFAAGDVDRKGLRQIVTATGDSIAAQ 300

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QY 300 SAAEYIEHLNDQARS 314
: ||||| : :
Db 301 NVQHYIEELAERKVN 315

RESULT 9
Q89YJ7 PRELIMINARY; PRT; 312 AA.
ID Q89YJ7
AC Q89YJ7
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Thioredoxin reductase (NADPH) (EC 1.6.4.5).
DE TRXB1 OR LP 0761.
GN Lactobacillus plantarum.
OS Lactobacillales; Lactobacillaceae;
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Enterococcus.
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerberem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer K., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR GO: 00015036; F:disulfide oxidoreductase activity; IEA.
DR GO: 0006118; P:electron transport; IEA.
DR InterPro: IPR001327; FAD pyr_reduct.
DR InterPro: IPR002025; NAD_88.
DR InterPro: IPR000103; Pyridine_reduct_2.
DR InterPro: IPR001100; Pyr_reduct.
DR InterPro: IPR008255; Pyr_reduct_2 AS.
DR InterPro: IPR003042; Rng_mnoxigenase.
DR Pfam: PF00070; Pyr_reduct_1.
DR PRINTS: PR00419; ADXBDTASE.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00411; PNDRTASEII.
DR PRINTS: PR00469; PNDRTASEII.
DR PROSITE: PS00573; PYRIDINE_REDOX_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 312 AA; 33455 MW; BF013DD361ED8343 CRC64;

Query Match 56.7%; Score 943; DB 16; Length 312;
Best Local Similarity 55.5%; Pred. No. 4.9e-59;
Matches 171; Conservative 54; Mismatches 83; Indels 0; Gaps 0;

QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 66
: ||||| : :
Db 5 YDVIIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 64
: ||||| : :

QY 67 KMFHAKFGAVYQGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAAYKKIGVPGBOE 126
: ||||| : :
Db 65 DMYESATQGAAYAGSVESVEDRGDKVITVTDSTTFETKALVIGTGEYKLGVTGDT 124
: ||||| : :

QY 127 LGGRGVSYCAVCDGAPFFKNKRLFVIGGSDSAVEEGTFTTKADKVTIHRDELRAQRI 186
: ||||| : :
Db 125 YGGRGVSYCAVCDGAPFFKNKRLVWVGSDSAVEEGTFTTKADKVTIHRDELRAQRI 184
: ||||| : :

QY 187 QDRAFNKIDFIWSHHTKTSINEKDGKGSVTLTSTKGSSEETHEADGVFIYGMKPLTA 246
: ||||| : :
Db 185 QDRAFNKIDFIWSHHTKTSINEKDGKGSVTLTSTKGSSEETHEADGVFIYGMKPLTA 244
: ||||| : :

QY 247 PFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDGSAIAQSAAYIE 306
: ||||| : :
Db 245 PFSNLGITDENGWIEIHNHETKVPGLFAVGDRKKDLQVATAVGCGTAGGVVYIT 304
: ||||| : :

QY 307 HLNDQARS 314
: ||||| : :
Db 305 ALGDKNVN 312

RESULT 10
Q835N8 PRELIMINARY; PRT; 304 AA.
ID Q835N8
AC Q835N8
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Thioredoxin reductase.
DE TRXB OR EF1338.
GN Enterococcus faecalis (Streptococcus faecalis).
OS Enterococcus faecalis; Lactobacillales; Enterococcaceae; Enterococcus.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=2250857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.P.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Madupu R., Nelson W.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Shetty J., Khouri H.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Fraser C.M.,
RA Uterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL: AE016951; AAC081129.1; -.
DR TIGR: EF1338; -.
DR GO: 0005737; C:cytoplasm; IEA.
DR GO: 00015036; F:disulfide oxidoreductase activity; IEA.
DR GO: 0004791; F:thioredoxin-disulfide reductase activity; IEA.
DR GO: 0006118; P:electron transport; IEA.
DR GO: 0019430; P:removal of superoxide radicals; IEA.
DR InterPro: IPR000759; Adrnx reductase.
DR InterPro: IPR001327; FAD pyr_reduct.
DR InterPro: IPR00103; Pyridine_reduct_2.
DR InterPro: IPR001100; Pyr_reduct.
DR InterPro: IPR008255; Pyr_reduct_2 AS.
DR InterPro: IPR005982; Thioredox_reduct.
DR Pfam: PF00070; Pyr_reduct_1.
DR PRINTS: PR00419; ADXBDTASE.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00411; PNDRTASEII.
DR PRINTS: PR00469; PNDRTASEII.
DR PRODOM: PD000139; FAD pyr_reduct; 1.
DR TIGRFAMs: TIGR01292; TRX reduct; 1.
DR PROSITE: PS00573; PYRIDINE_REDOX_2; 1.
KW Complete proteome.
SQ SEQUENCE 304 AA; 33240 MW; F08B31A3E28628EE CRC64;

Query Match 56.6%; Score 940; DB 16; Length 304;
Best Local Similarity 58.9%; Pred. No. 7.7e-59;
Matches 178; Conservative 42; Mismatches 82; Indels 0; Gaps 0;

QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 66
: ||||| : :
Db 2 YDVIIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 61
: ||||| : :

QY 67 KMFHAKFGAVYQGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAAYKKIGVPGBOE 126
: ||||| : :
Db 62 KNYENVERKFTENAIGVINGIEDHGSYKEVICDDKSYEAKAVIATGCEHRKLGKVGEE 121
: ||||| : :

QY 127 LGGRGVSYCAVCDGAPFFKNKRLFVIGGSDSAVEEGTFTTKADKVTIHRDELRAQRI 186
: ||||| : :
Db 122 FAGRGVSYCAVCDGAPFFKNKRLVWVGSDSAVEEAIYLTQFASVVVYHRDELRAQRI 181
: ||||| : :

QY 187 QDRAFNKIDFIWSHHTKTSINEKDGKGSVTLTSTKGSSEETHEADGVFIYGMKPLTA 246
: ||||| : :

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Db 182 QDFAFANEKISFVWDVTVEEVGNEMVVTGKARNVKTEVSEIANGVFYIVGLDPLTE 241
QY 247 PFKDLGINTDYGIVTKDDMTTSVPGIPAAAGVDRKGLRQIVTATGDSIAAQAASAEYIE 306
Db 242 PFKAGITNEAGWLETQEMTKIPGVYAGVDRKILRQITAVGEGGIAGQOVFNYYIE 301
QY 307 HL 308
Db 302 EL 303

RESULT 11
Q8NZY5
ID Q8NZY5 PRELIMINARY; PRT; 305 AA.
AC Q8NZY5
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thiorodoxin reductase.
DE Thiorodoxin reductase.
GN TRXB OR SPYM18.1666.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gorpel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.B., Rickles S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AB010078; AAL98210.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004791; F:thiorodoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrxn_reductase.
DR InterPro; IPR001327; FAD_pyr_redux.
DR InterPro; IPR001003; Pyridine_redux_2.
DR InterPro; IPR001100; Pyr_redux.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR InterPro; IPR005982; Thiorodox_reduct.
DR Pfam; PF00070; Pyr_redux; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRfams; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 33444 MW; 52785BAF746BFF9D CRC64;

Query Match 54.1%; Score 899; DB 16; Length 305;
Best Local Similarity 56.3%; Pred. No. 6.3e-56;
Matches 169; Conservative 49; Mismatches 82; Indels 0; Gaps 0;

QY 7 FDIATIGAPGAGTAAVYASRANLTKVTMIERGIPGGOMANTEEVNFGFEMITGPDIST 66
Db 2 YDTLIIGSPAGMTAALYAARSNLVAIEQAPGGQWNTFDIENPGYDHISGPELAM 61
QY 67 KNFEHAKFGAVYQVGDITKSVEDKGEYKVINFGNKLTAKAVIATGAAYKKIGVPGEOE 126
Db 62 KMYEPLKFNVENIYGVQKIENFGDKVCLTSDASYEAKVTIATGAKYVLVPGGEY 121
QY 127 LGGRGVSYCAVDCGAGFFKKNKRLFVLGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 186
Db 122 YTSRGVSYCAVDCGAGFFRQDQLLVVGGGDSAVEEAIYLTQFAKVTIVHRRDQLRAQKIL 181

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QY 187 QDRAFKNDKIDFIWHTTKSINERKDGKGVSVTLSTKDGSEETHEADGVFIYIGMKPLTA 246
Db 182 QDRAFANDKVDFIWDSVVKEIQGNIDIKSVNLINVKTGQVTDHAFGCVFIYVGMNPTIG 241
QY 247 PFKDLGINTDYGIVTKDDMTTSVPGIPAAAGVDRKGLRQIVTATGDSIAAQAASAEYIE 306
Db 242 MVKDLITDSEGWIITDDHMRITSPGIFAIGVDRKQLRQITAVGDAIAGQGVVHYLE 301

RESULT 12
Q8K6D2
ID Q8K6D2 PRELIMINARY; PRT; 305 AA.
AC Q8K6D2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative thiorodoxin reductase (putative NADH oxidase/alkyl
DE hydroperoxidase reductase).
GN NOX.2 OR SPYM3.1395 OR SPS0467.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014163; AAM80002.1; -
DR GO; GO:0005142; BAC63562.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0004791; F:thiorodoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrxn_reductase.
DR InterPro; IPR001327; FAD_pyr_redux.
DR InterPro; IPR001003; Pyridine_redux_2.
DR InterPro; IPR001100; Pyr_redux.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR InterPro; IPR005982; Thiorodox_reduct.
DR Pfam; PF00070; Pyr_redux; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRfams; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Hypothetical protein; Peroxidase; Complete proteome.
SQ SEQUENCE 305 AA; 33543 MW; 3F947A628769E8BB CRC64;

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Query Match

54.0%; Score 897; DB 16; Length 305;

Best Local Similarity 56.3%; Pred. No. 8.7e-56;

Matches 169; Conservative 49; Mismatches 82; Indels 0; Gaps 0;

QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPFGFEMITGPDLS 66
DB 2 YDTLIIGSGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPFGFEMITGPDLS 61
QY 67 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGBOE 126
DB 62 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGBOE 121
QY 127 LGGRGVSYCAVCDGAFKKRNLKRVIGGDSAVBEFTTKFADKVTIVHRRDELRAQRL 186
DB 122 YNSRGVSYCAVCDGAFKKRNLKRVIGGDSAVBEFTTKFADKVTIVHRRDELRAQRL 181
QY 187 QDRAFKNDKIDFTWSHTTKSINBKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA 246
DB 122 YNSRGVSYCAVCDGAFKKRNLKRVIGGDSAVBEFTTKFADKVTIVHRRDELRAQRL 181
QY 187 QDRAFKNDKIDFTWSHTTKSINBKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA 246
DB 182 QDRAFAFANDKIDFTWSHTTKSINBKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA 241
QY 247 PFKDLGITNDVGVYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAAASAAEYIE 306
DB 242 MVKDLGITNDVGVYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAAASAAEYIE 301

RESULT 13
Q8DVL7 PRELIMINARY; PRT; 304 AA.

AC Q8DVL7; 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative thioredoxin reductase (NADPH) (EC 1.6.4.5).
GN TRXB OR SMU.463.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAI159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.,
RT "Genome sequence of *Streptococcus mutans* UAI59, a cariogenic dental
pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL; AE014892; AAN58212.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrxn reductase.
DR InterPro; IPR001327; FAD pyr redox.
DR InterPro; IPR001100; Pyr redox.
DR InterPro; IPR008255; Pyr_redox2_AS.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF00070; pyr_redox; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRfams; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE REDOX_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 304 AA; 33117 MW; CEF7BEC1B8E0A50F CRC64;

Query Match 53.1%; Score 882; DB 16; Length 304;
Best Local Similarity 55.2%; Pred. No. 1e-54;
Matches 165; Conservative 52; Mismatches 82; Indels 0; Gaps 0;
QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPFGFEMITGPDLS 66
DB 2 YDTLIIGSGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPFGFEMITGPDLS 61

QY 67 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGBOE 126
DB 62 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGBOE 121
QY 127 LGGRGVSYCAVCDGAFKKRNLKRVIGGDSAVBEFTTKFADKVTIVHRRDELRAQRL 186
DB 122 YNSRGVSYCAVCDGAFKKRNLKRVIGGDSAVBEFTTKFADKVTIVHRRDELRAQRL 181
QY 187 QDRAFKNDKIDFTWSHTTKSINBKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA 246
DB 182 QDRAFAFANDKIDFTWSHTTKSINBKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA 241
QY 247 PFKDLGITNDVGVYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAAASAAEYIE 305
DB 242 MVKDLGITNDVGVYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAAASAAEYIE 300

RESULT 14
Q9CH02 PRELIMINARY; PRT; 308 AA.

AC Q9CH02; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thioredoxin reductase (EC 1.6.4.5).
GN TRXB1 OR LL0940.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753 (2001).
CC -!- COFACTOR: FAD (BY SIMILARITY).
DR EMBL; AE006328; AAK05038.1; -.
DR PIR; D86742; D86742.
DR HSSP; Q39243; 1VDC.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrxn reductase.
DR InterPro; IPR001327; FAD pyr redox.
DR InterPro; IPR001100; Pyr redox.
DR InterPro; IPR008255; Pyr_redox2_AS.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF00070; pyr_redox; 1.
DR PRINTS; PR00419; ADXRDASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRfams; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE REDOX_2; 1.
KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 308 AA; 33894 MW; 363397A925E48267 CRC64;

Query Match 52.5%; Score 872; DB 16; Length 308;
Best Local Similarity 53.1%; Pred. No. 5.3e-54;
Matches 163; Conservative 54; Mismatches 90; Indels 0; Gaps 0;
QY 3 TEIDFIIAGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPFGFEMITG 62
DB 2 TEKYDVVIGSGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPFGFEMITG 61
QY 63 DLSTKMFHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAAYKKIGV 122

Db 62 ELSMKMAEPLGGLGVENAYGFVTAIEDHGYKKIITTEDEFVTKSIIITATGANHRKLEIP 121
 Qy 123 GEQELGGRGVSYCAVCDGAFKFNKRLFVIGGDSAVESGTTTFKPADKVTVIHRDELRA 182
 Db 122 GEEYVARGVSYCAVCDGAFKFNQELFVIGGDSAVEEALYTRFGQSVTTHRRDKLRA 181
 Qy 183 QRILQDRAFNKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSEETHEADGVFTYIGMK 242
 Db 182 QEIIQORAFKEKINFWDSPMEIKGDDKKVQSVVKNVKTGEVTEKAFGGIIFYVGLD 241
 Qy 243 PLTAPFDKLGITNDVGYITVTKDDMTTSVPGIPAGDVRDKGLRQIVTATGDSIAAQSAA 302
 Db 242 PVAEFAGNLGTDGAGWIIITDHRMTSLPGIFAVGDVRQKDFRQITTAIGDGAQAQZAY 301
 Qy 303 EYIEHLN 309
 Db 302 KFVAELD 308

RESULT 15

Q8E773 PRELIMINARY; PRT; 304 AA.
 AC Q8E773;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN GBS0284.
 OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEM316 / Serotype III;
 RX MEDLINE=2242508; PubMed=12354221;
 RA Glaser P., Zouinok C., Buchrieser C., Chevalier P., Frangeul L.,
 RA Meadek T., Rousine M., Couve E., Lalloui L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513 (2002).
 DR EMBL; AL766844; CAD45929.1; -;
 DR Sagalinst; gbs0284; -;
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrxndx reductase.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR00103; Pyridine redox_2.
 DR InterPro; IPR001100; Pyr redox.
 DR InterPro; IPR008255; Pyr_redox2_AS.
 DR InterPro; IPR005982; Thioredox_reduct.
 DR Pfam; PF00070; pyr_redox; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNRDRTASEI.
 DR PRINTS; PR00459; PNRDRTASEII.
 DR TIGRFAMs; TIGR01292; TRX reduct; 1.
 DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 304 AA; 33123 MW; 4B6B55E55FB84E8D CRC64;

Query Match 51.3%; Score 852.5; DB 16; Length 304;
 Best Local Similarity 53.3%; Pred. NO. 1.3e-52;
 Matches 161; Conservative 57; Mismatches 83; Indels 1; Gaps 1;
 Qy 7 FDIATIGAGPAGTAAYVSRANLKTVMIERGIPCGQMANTVEENPFPGFEMITGPDLST 66
 2 YDTLIIGSGPGMTAALYAARSLKVLIEQAFPGQGMNTAEIENYPGYDHISGPGLSM 61

Qy 67 KMFPHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAEEKIGVPGBOE 126
 Db 62 KMYEPLEKFEVEHIYGIQVRVENDGDVYKRVITEDSEYAKTVIATGAKNSLLGVFGBEE 121
 Qy 127 LGGEGVSYCAVCDGAFKFNKRLFVIGGDSAVEEGTFTTKPADKVTVIHRDELRAQRIIL 186
 Db 122 YTSRGVSYCAVCDGAFKFNQELFVIGGDSAVEEAVFLTQFAKSVTIIHRDQLRAQKVL 181
 Qy 187 QDRAFNKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSEETHEADGVFTYIGMKPLTA 246
 Db 182 QDRAFANEKIFVWDSPVMEIKGNEIKVSGVTVENLKTGEISEMTFGGVFTYVGLKPHSS 241
 Qy 247 PFKDLGITNDVGYITVTKDDMTTSVPGIPAGDVRDKGLRQIVTATGDSIAAQAEEVI - 305
 Db 242 MVSELGITDETGWLTDTNMTKTSIPGLIYALGDVVRQKDLRQIATAVGGAIAQGVYNYIT 301
 Qy 306 EH 307
 Db 302 EH 303

Search completed: September 15, 2004, 12:20:47
 Job time : 118 secs

